

STN SEARCH HISTORY

FILE 'MEDLINE, BIOSIS, PROMT, SCISEARCH, CAPLUS' ENTERED AT 22:16:05 ON
20 JUL 2006

L1 80110 SEA (HYDROGEN OR H2) (3A) (PRODUC? OR EVOLV? OR GENERAT?)
L2 942 SEA L1 AND (ALGAE OR ALGA OR ALGAL OR CHLAMYDOMONAS OR
REINHARDTII)
L3 24 SEA L2 AND (IRON (A) HYDROGENASE)
L4 14 DUP REM L3 (10 DUPLICATES REMOVED)
L5 5 SEA L4 AND PY<2003
D L5, IBIB ABS, 1-5
L6 39 SEA L2 AND (FE (A) HYDROGENASE)
L7 17 DUP REM L6 (22 DUPLICATES REMOVED)
L8 6 SEA L7 AND PY<2003
L9 4 SEA L8 NOT L5
D L9, IBIB ABS, 1-4

BEST AVAILABLE COPY

STN SEARCH HISTORY

(FILE 'HOME' ENTERED AT 13:21:51 ON 20 JUL 2006)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:24:27 ON 20 JUL 2006
SEA ((HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?))

39 FILE ADISCTI
10 FILE ADISINSIGHT
12 FILE ADISNEWS
967 FILE AGRICOLA
384 FILE ANABSTR
302 FILE ANTE
544 FILE AQUALINE
509 FILE AQUASCI
1088 FILE BIOENG
9052 FILE BIOSIS
1644 FILE BIOTECHABS
1644 FILE BIOTECHDS
1923 FILE BIOTECHNO
2648 FILE CABA
42097 FILE CAPLUS
3271 FILE CEABA-VTB
1425 FILE CIN
763 FILE CONFSCI
10 FILE CROPB
98 FILE CROPU
60 FILE DDFB
383 FILE DDFU
1207 FILE DGENE
1487 FILE DISSABS
60 FILE DRUGB
634 FILE DRUGU
72 FILE EMBAL
5874 FILE EMBASE
2864 FILE ESBIODBASE
1 FILE FOREGE
463 FILE FROSTI
268 FILE FSTA
25321 FILE GENBANK
116 FILE HEALSAFE
15648 FILE IFIPAT
6 FILE IMSDRUGNEWS
8 FILE IMSRESEARCH
4487 FILE JICST-EPLUS
33 FILE KOSMET
2234 FILE LIFESCI
6006 FILE MEDLINE
4943 FILE NTIS
124 FILE OCEAN
8640 FILE PASCAL
14 FILE PCTGEN
8 FILE PHAR
24 FILE PHARMAML
1 FILE PHIC
60 FILE PHIN
8248 FILE PROMT
10 FILE PROUSDDR
109 FILE RDISCLOSURE
14681 FILE SCISEARCH
10 FILE SYNTHLINE
8353 FILE TOXCENTER
62365 FILE USPATFULL

6028 FILE USPAT2
2 FILE VETB
51 FILE VETU
555 FILE WATER
24599 FILE WPIDS
184 FILE WPIFV
24599 FILE WPINDEX

L1 QUE ((HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?))

FILE 'MEDLINE, BIOSIS, PROMT, SCISEARCH, CAPLUS' ENTERED AT 13:31:07 ON
20 JUL 2006

L2 80084 S (HYDROGEN OR H2) (3A) (PRODUC? OR GENERAT? OR EVOLV?)
L3 1392 S L2 AND (MUTAT? OR MUTEIN OR MUTAG? OR MUTANT)
L4 17 S L3 AND ((IRON OR FE) (A)HYDROGENASE)
L5 13 DUP REM L4 (4 DUPLICATES REMOVED)
L6 4 S L5 AND PY<2003

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	10	"5871952"	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 21:50
L2	2	"6180406".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 21:51
L3	1113	light-induced adj promoter	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 21:52
L4	1051	I3 and Chlamydomonas	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 21:52
L5	1	I4 and (hydrogen adj production)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:08
L6	71185	((hydrogen or H2) adj3 (produc\$4 or generat\$4 or evolv\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:09
L7	955	L6 and (algae or algal or alga)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:10
L8	50	I7 and (Chlamydomonas or reinhardtii)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:10
L9	48	L8 and (process or method)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:10
L10	13	L9 and ferredoxin	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:11
L11	22	L9 and hydrogenase	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:11

EAST Search History

L12	11	l11 not l10	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:11
L13	1135	seibert.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:12
L14	19	L13 and l6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 22:12

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"4476105".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 11:31
L2	66906	hydrogen adj3 (produc\$4 or generat\$ or photoproduc\$4 or synthesi\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 11:33
L3	1045	I2 and (cell adj3 (electroporat\$4 or transform\$4 or transfect\$4 or inject\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 11:34
L4	779	I3 and (method SAME (screen\$4 or identif\$4 or select\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 11:35
L5	840	I3 and ((method or process) SAME (screen\$4 or identif\$4 or select\$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 11:36
L6	3	I5 and ((iron or Fe) adj hydrogenase)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 12:04
L7	613	I5 and oxygen	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 12:04
L8	168	L5 and (algae or alga or algal)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 12:05
L9	18	L8 and (green adj alg\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	ON	2006/07/20 13:01

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rup.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:19:13 ; Search time 131.333 Seconds
(without alignments)
56.346 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	29	100.0	219	2 Q66870_9CALI	Q66870 feline cali
2	28	96.6	87	2 Q8P6G5_XANCP	Q8p6g5 xanthomonas
3	28	96.6	191	2 Q445P9_SOLUS	Q445p9 solibacter
4	28	96.6	273	2 Q4KG49_PSEF5	Q4kg49 pseudomonas

5	28	96.6	319	2	Q5V4C1_HALMA	Q5v4c1 haloarcula
6	28	96.6	414	2	Q93231_CAEEL	Q93231 caenorhabdi
7	28	96.6	516	2	Q564C3_BIFAN	Q564c3 bifidobacte
8	28	96.6	749	2	Q6BZD2_DEBHA	Q6bzd2 debaryomyce
9	28	96.6	817	2	Q6ZPN1_MOUSE	Q6zpn1 mus musculu
10	28	96.6	826	2	Q8IY15_HUMAN	Q8iy15 homo sapien
11	28	96.6	921	2	Q61SM7_CAEER	Q61sm7 caenorhabdi
12	28	96.6	969	2	Q7UM46_RHOBA	Q7um46 rhodopirell
13	28	96.6	1546	2	Q3WJS0_9ACTO	Q3wjs0 frankia sp.
14	28	96.6	1727	2	Q68FD9_MOUSE	Q68fd9 mus musculu
15	28	96.6	1865	2	Q9HCM3_HUMAN	Q9hcm3 homo sapien
16	28	96.6	3463	2	Q7R1E2_GIALA	Q7rle2 giardia lam
17	27	93.1	84	2	Q5RVY2_9HIV1	Q5rvy2 human immun
18	27	93.1	85	2	Q5RVP5_9HIV1	Q5rvp5 human immun
19	27	93.1	86	2	Q5RUR7_9HIV1	Q5rur7 human immun
20	27	93.1	94	2	Q7SJ42_9HIV1	Q7sj42 human immun
21	27	93.1	94	2	Q7SJ70_9HIV1	Q7sj70 human immun
22	27	93.1	94	2	Q7SJ73_9HIV1	Q7sj73 human immun
23	27	93.1	94	2	Q7SJA0_9HIV1	Q7sja0 human immun
24	27	93.1	94	2	Q7SJB5_9HIV1	Q7sjb5 human immun
25	27	93.1	94	2	Q7SJG2_9HIV1	Q7sjg2 human immun
26	27	93.1	96	2	Q6UIH6_9HIV1	Q6uih6 human immun
27	27	93.1	98	2	Q58RR3_9HIV1	Q58rr3 human immun
28	27	93.1	98	2	Q5RX46_9HIV1	Q5rx46 human immun
29	27	93.1	98	2	Q9DPX2_9HIV1	Q9dpx2 human immun
30	27	93.1	99	2	O09859_9HIV1	O09859 human immun
31	27	93.1	99	2	O09860_9HIV1	O09860 human immun
32	27	93.1	99	2	O09861_9HIV1	O09861 human immun
33	27	93.1	99	2	O09862_9HIV1	O09862 human immun
34	27	93.1	99	2	O09863_9HIV1	O09863 human immun
35	27	93.1	99	2	O09865_9HIV1	O09865 human immun
36	27	93.1	99	2	O09867_9HIV1	O09867 human immun
37	27	93.1	99	2	O09868_9HIV1	O09868 human immun
38	27	93.1	99	2	O09869_9HIV1	O09869 human immun
39	27	93.1	99	2	O09871_9HIV1	O09871 human immun
40	27	93.1	99	2	O09950_9HIV1	O09950 human immun
41	27	93.1	99	2	O09951_9HIV1	O09951 human immun
42	27	93.1	99	2	O09952_9HIV1	O09952 human immun
43	27	93.1	99	2	O09953_9HIV1	O09953 human immun
44	27	93.1	99	2	O09954_9HIV1	O09954 human immun
45	27	93.1	99	2	O09955_9HIV1	O09955 human immun
46	27	93.1	99	2	O09956_9HIV1	O09956 human immun
47	27	93.1	99	2	O10196_9HIV1	O10196 human immun
48	27	93.1	99	2	O10201_9HIV1	O10201 human immun
49	27	93.1	99	2	O10215_9HIV1	O10215 human immun
50	27	93.1	99	2	O38681_9HIV1	O38681 human immun
51	27	93.1	99	2	O38686_9HIV1	O38686 human immun
52	27	93.1	99	2	Q58RN9_9HIV1	Q58rn9 human immun
53	27	93.1	99	2	Q58RS6_9HIV1	Q58rs6 human immun
54	27	93.1	99	2	Q58RS8_9HIV1	Q58rs8 human immun
55	27	93.1	99	2	Q5RT92_9HIV1	Q5rt92 human immun
56	27	93.1	99	2	Q5RTF3_9HIV1	Q5rtf3 human immun
57	27	93.1	99	2	Q5RTF9_9HIV1	Q5rtf9 human immun
58	27	93.1	99	2	Q5RTG5_9HIV1	Q5rtg5 human immun
59	27	93.1	99	2	Q5RTH8_9HIV1	Q5rth8 human immun
60	27	93.1	99	2	Q5RTS8_9HIV1	Q5rts8 human immun
61	27	93.1	99	2	Q5RUB4_9HIV1	Q5rub4 human immun
62	27	93.1	99	2	Q5RUB5_9HIV1	Q5rub5 human immun
63	27	93.1	99	2	Q5RUC6_9HIV1	Q5ruc6 human immun
64	27	93.1	99	2	Q5RUY4_9HIV1	Q5rui4 human immun
65	27	93.1	99	2	Q5RUY5_9HIV1	Q5rui5 human immun

66	27	93.1	99	2	Q5RVM1_9HIV1	Q5rvm1	human	immun
67	27	93.1	99	2	Q5RVP4_9HIV1	Q5rvp4	human	immun
68	27	93.1	99	2	Q5RVP6_9HIV1	Q5rvp6	human	immun
69	27	93.1	99	2	Q5RW30_9HIV1	Q5rw30	human	immun
70	27	93.1	99	2	Q5RW31_9HIV1	Q5rw31	human	immun
71	27	93.1	99	2	Q5RW32_9HIV1	Q5rw32	human	immun
72	27	93.1	99	2	Q5RW91_9HIV1	Q5rw91	human	immun
73	27	93.1	99	2	Q5RW92_9HIV1	Q5rw92	human	immun
74	27	93.1	99	2	Q5RWA2_9HIV1	Q5rwa2	human	immun
75	27	93.1	99	2	Q5RWA5_9HIV1	Q5rwa5	human	immun
76	27	93.1	99	2	Q5RWP2_9HIV1	Q5rwp2	human	immun
77	27	93.1	99	2	Q5RWS6_9HIV1	Q5rws6	human	immun
78	27	93.1	99	2	Q5RX44_9HIV1	Q5rx44	human	immun
79	27	93.1	99	2	Q5RX45_9HIV1	Q5rx45	human	immun
80	27	93.1	99	2	Q5RX59_9HIV1	Q5rx59	human	immun
81	27	93.1	99	2	Q5RX60_9HIV1	Q5rx60	human	immun
82	27	93.1	99	2	Q5RX91_9HIV1	Q5rx91	human	immun
83	27	93.1	99	2	Q5RXR9_9HIV1	Q5rxr9	human	immun
84	27	93.1	99	2	Q5RYB1_9HIV1	Q5ryb1	human	immun
85	27	93.1	99	2	Q5RYC4_9HIV1	Q5ryc4	human	immun
86	27	93.1	99	2	Q5RYF1_9HIV1	Q5ryf1	human	immun
87	27	93.1	99	2	Q5RYF2_9HIV1	Q5ryf2	human	immun
88	27	93.1	99	2	Q5RYF3_9HIV1	Q5ryf3	human	immun
89	27	93.1	99	2	Q6Q042_9HIV1	Q6q042	human	immun
90	27	93.1	99	2	Q6REF0_9HIV1	Q6ref0	human	immun
91	27	93.1	99	2	Q6SMF9_9HIV1	Q6smf9	human	immun
92	27	93.1	99	2	Q6UIH5_9HIV1	Q6uih5	human	immun
93	27	93.1	99	2	Q6UIH7_9HIV1	Q6uih7	human	immun
94	27	93.1	99	2	Q7SPI1_9HIV1	Q7spi1	human	immun
95	27	93.1	99	2	Q7SQC0_9HIV1	Q7sqc0	human	immun
96	27	93.1	99	2	Q7SQC3_9HIV1	Q7sqc3	human	immun
97	27	93.1	99	2	Q7ZCK3_9HIV1	Q7zck3	human	immun
98	27	93.1	99	2	Q7ZCK4_9HIV1	Q7zck4	human	immun
99	27	93.1	99	2	Q7ZCK5_9HIV1	Q7zck5	human	immun
100	27	93.1	99	2	Q7ZCK6_9HIV1	Q7zck6	human	immun
101	27	93.1	99	2	Q7ZCK7_9HIV1	Q7zck7	human	immun
102	27	93.1	99	2	Q7ZCK8_9HIV1	Q7zck8	human	immun
103	27	93.1	99	2	Q7ZCK9_9HIV1	Q7zck9	human	immun
104	27	93.1	99	2	Q7ZCL0_9HIV1	Q7zcl0	human	immun
105	27	93.1	99	2	Q7ZCL2_9HIV1	Q7zcl2	human	immun
106	27	93.1	99	2	Q7ZPC8_9HIV1	Q7zpc8	human	immun
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108	27	93.1	99	2	Q8ANG8_9HIV1	Q8ang8	human	immun
109	27	93.1	99	2	Q8ANI7_9HIV1	Q8ani7	human	immun
110	27	93.1	99	2	Q8ANJ2_9HIV1	Q8anj2	human	immun
111	27	93.1	99	2	Q8ANJ8_9HIV1	Q8anj8	human	immun
112	27	93.1	99	2	Q8ANK2_9HIV1	Q8ank2	human	immun
113	27	93.1	99	2	Q8ANK4_9HIV1	Q8ank4	human	immun
114	27	93.1	99	2	Q8ANN9_9HIV1	Q8ann9	human	immun
115	27	93.1	99	2	Q8ANP9_9HIV1	Q8anp9	human	immun
116	27	93.1	99	2	Q8ANT3_9HIV1	Q8ant3	human	immun
117	27	93.1	99	2	Q8ANZ2_9HIV1	Q8anz2	human	immun
118	27	93.1	99	2	Q8UNX0_9HIV1	Q8unx0	human	immun
119	27	93.1	99	2	Q99D67_9HIV1	Q99d67	human	immun
120	27	93.1	99	2	Q99EZ3_9HIV1	Q99ez3	human	immun
121	27	93.1	99	2	Q9E105_9HIV1	Q9e105	human	immun
122	27	93.1	99	2	Q9E112_9HIV1	Q9e112	human	immun
123	27	93.1	99	2	Q9E113_9HIV1	Q9e113	human	immun
124	27	93.1	99	2	Q9E3P2_9HIV1	Q9e3p2	human	immun
125	27	93.1	99	2	Q9ILQ2_9HIV1	Q9ilq2	human	immun
126	27	93.1	99	2	Q9ILU4_9HIV1	Q9ilu4	human	immun

127	27	93.1	99	2	Q9J017_9HIV1	Q9j017 human immun
128	27	93.1	99	2	Q9J018_9HIV1	Q9j018 human immun
129	27	93.1	99	2	Q9JAN4_9HIV1	Q9jan4 human immun
130	27	93.1	99	2	Q9JAN5_9HIV1	Q9jan5 human immun
131	27	93.1	99	2	Q9JAN6_9HIV1	Q9jan6 human immun
132	27	93.1	99	2	Q9JAN7_9HIV1	Q9jan7 human immun
133	27	93.1	99	2	Q9JAN8_9HIV1	Q9jan8 human immun
134	27	93.1	99	2	Q9JAN9_9HIV1	Q9jan9 human immun
135	27	93.1	99	2	Q9JAP0_9HIV1	Q9jap0 human immun
136	27	93.1	99	2	Q9JAP1_9HIV1	Q9jap1 human immun
137	27	93.1	99	2	Q9JAP2_9HIV1	Q9jap2 human immun
138	27	93.1	99	2	Q9JAP4_9HIV1	Q9jap4 human immun
139	27	93.1	99	2	Q9JAP5_9HIV1	Q9jap5 human immun
140	27	93.1	100	2	Q58RS1_9HIV1	Q58rs1 human immun
141	27	93.1	100	2	Q5MHI0_9HIV1	Q5mhi0 human immun
142	27	93.1	100	2	Q6QJW4_9HIV1	Q6qjw4 human immun
143	27	93.1	106	2	Q8Q3D8_9HIV1	Q8q3d8 human immun
144	27	93.1	118	2	Q70VT4_9HIV1	Q70vt4 human immun
145	27	93.1	143	2	Q3MGN0_ANAVT	Q3mgn0 anabaena va
146	27	93.1	144	2	Q8YUC8_ANASP	Q8yuc8 anabaena sp
147	27	93.1	156	2	Q5Y8C9_9CLOT	Q5y8c9 clostridium
148	27	93.1	156	2	Q68YU5_9CLOT	Q68yu5 uncultured
149	27	93.1	156	2	Q68YV3_9CLOT	Q68yv3 uncultured
150	27	93.1	156	2	Q68YV4_9CLOT	Q68yv4 uncultured

ALIGNMENTS

RESULT 1

Q66870_9CALI

ID Q66870_9CALI PRELIMINARY; PRT; 219 AA.

AC Q66870;

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Capsid protein (Fragment).

OS Feline calicivirus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;

OC Vesivirus.

OX NCBI_TaxID=11978;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FS;

RX MEDLINE=95028111; PubMed=7941699; DOI=10.1016/0168-1702(94)90016-7;

RA Seal B.S.;

RT "Analysis of capsid protein gene variation among divergent isolates of

RT feline calicivirus.";

RL Virus Res. 33:39-53(1994).

CC

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CC

DR EMBL; U06650; AAA67210.1; -; Genomic_RNA.

DR InterPro; IPR004005; Calici_coat.

DR Pfam; PF00915; Calici_coat; 1.

FT NON_TER 1 1

FT NON_TER 219 219

SQ SEQUENCE 219 AA; 23926 MW; E403FECF5C022469 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 219;

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This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763712
[start](#)

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:24:08 ; Search time 15.6667 Seconds
(without alignments)
49.132 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	96.6	386	2	T19354	hypothetical prote
2	27	93.1	144	2	AI2108	hypothetical prote
3	27	93.1	290	2	H96982	L-serine dehydrata
4	27	93.1	382	2	JC2571	cellulase (EC 3.2.
5	27	93.1	574	1	HQCL1P	hydrogenase (EC 1.
6	27	93.1	582	2	D96903	hydrogene dehydrog
7	27	93.1	582	2	JC6002	hydrogenase (EC 1.
8	27	93.1	585	2	D57150	hydrogenase (EC 1.

9	27	93.1	608	2	C72405	hydrogenase (EC 1.
10	27	93.1	1206	2	T18557	probable hydrogenase
11	27	93.1	4096	2	A57099	DNA-activated prot
12	26	89.7	99	2	S63716	HIV-1 retropepsin
13	26	89.7	100	2	S63708	HIV-1 retropepsin
14	26	89.7	106	2	S63756	HIV-1 retropepsin
15	26	89.7	113	4	S34484	retropepsin (EC 3.
16	26	89.7	115	2	S63741	HIV-1 retropepsin
17	26	89.7	122	2	S63749	HIV-1 retropepsin
18	26	89.7	123	2	S63744	HIV-1 retropepsin
19	26	89.7	126	2	S63738	HIV-1 retropepsin
20	26	89.7	129	2	S63740	HIV-1 retropepsin
21	26	89.7	129	2	S63739	HIV-1 retropepsin
22	26	89.7	130	2	S63754	HIV-1 retropepsin
23	26	89.7	131	2	A59365	ribosomal protein
24	26	89.7	132	2	S63733	HIV-1 retropepsin
25	26	89.7	133	2	S63736	HIV-1 retropepsin
26	26	89.7	143	2	S63735	HIV-1 retropepsin
27	26	89.7	145	2	S63745	HIV-1 retropepsin
28	26	89.7	149	2	S63734	HIV-1 retropepsin
29	26	89.7	154	2	S63751	HIV-1 retropepsin
30	26	89.7	160	2	S63753	HIV-1 retropepsin
31	26	89.7	166	2	S63752	HIV-1 retropepsin
32	26	89.7	176	2	S63747	HIV-1 retropepsin
33	26	89.7	294	2	S66041	conserved hypothet
34	26	89.7	297	2	D83825	hypothetical prote
35	26	89.7	298	2	F83652	superoxide-inducib
36	26	89.7	332	2	T42370	probable glucan 1,
37	26	89.7	403	2	H90487	alpha-fucosidase C
38	26	89.7	407	2	T39282	probable exo-beta-
39	26	89.7	421	1	HQDVFL	cytochrome-c3 hydr
40	26	89.7	421	1	HQDVLV	cytochrome-c3 hydr
41	26	89.7	463	2	JC2307	ribulose-bisphosph
42	26	89.7	786	2	H69980	single-strand DNA-
43	26	89.7	1002	1	GNLJND	HIV-1 retropepsin
44	26	89.7	1002	2	S54378	pol polyprotein -
45	26	89.7	1003	1	GNVWLTV	HIV-1 retropepsin
46	26	89.7	1003	1	B44001	HIV-1 retropepsin
47	26	89.7	1003	1	GNVWA2	HIV-1 retropepsin
48	26	89.7	1012	1	GNVWVL	HIV-1 retropepsin
49	26	89.7	1015	1	GNVWH3	HIV-1 retropepsin
50	26	89.7	1112	2	T02848	hsp70-related prot
51	26	89.7	1876	2	E97944	zinc metalloprotei
52	25	86.2	447	2	T40423	hypothetical prote
53	25	86.2	581	2	F97184	DNA modification m
54	25	86.2	668	2	JQ2356	capsid protein - f
55	25	86.2	716	1	C60008	RNA-directed RNA p
56	25	86.2	716	1	C60011	RNA-directed RNA p
57	25	86.2	716	1	P2IV34	RNA-directed RNA p
58	25	86.2	716	1	P2IV61	RNA-directed RNA p
59	25	86.2	716	1	P2IVWS	RNA-directed RNA p
60	25	86.2	716	1	P2IV68	RNA-directed RNA p
61	25	86.2	716	2	S07418	RNA-directed RNA p
62	25	86.2	1397	2	T51292	Dna2p - fission ye
63	25	86.2	1398	2	T39568	hypothetical helic
64	24	82.8	89	2	G70722	hypothetical prote
65	24	82.8	161	1	HMECA1	hemagglutinin AFA-
66	24	82.8	204	2	G83911	hypothetical prote
67	24	82.8	232	2	C95196	conserved hypothet
68	24	82.8	232	2	H98062	N-acetylmannosamin
69	24	82.8	232	2	C98021	N-acetylmannosamin

70	24	82.8	244	2	D86849	glutamate ABC tran
71	24	82.8	245	2	F64465	hypothetical prote
72	24	82.8	261	2	T25206	hypothetical prote
73	24	82.8	262	2	T05287	ribosomal protein
74	24	82.8	272	2	T01148	probable acetone-c
75	24	82.8	274	2	AB2325	hypothetical prote
76	24	82.8	290	2	T47991	hypothetical prote
77	24	82.8	313	2	E95113	proteinase maturat
78	24	82.8	313	2	D97982	proteinase maturat
79	24	82.8	324	2	T34148	hypothetical prote
80	24	82.8	342	2	C91176	probable heme/hemo
81	24	82.8	342	2	D86022	probable heme/hemo
82	24	82.8	400	2	T15459	hypothetical prote
83	24	82.8	428	2	H86890	hypothetical prote
84	24	82.8	442	1	UBUTB	tubulin beta chain
85	24	82.8	477	2	A28534	fatty-acyl-CoA red
86	24	82.8	506	2	F70617	probable aldehyde
87	24	82.8	526	2	S34945	nitrogenase (EC 1.
88	24	82.8	569	2	H87926	protein C17D12.7 [
89	24	82.8	607	2	F71094	probable aldehyde
90	24	82.8	653	2	D87602	sensory box histid
91	24	82.8	655	2	A54408	mannosyl-oligosacc
92	24	82.8	681	2	G90075	triacylglycerol li
93	24	82.8	682	2	S68970	triacylglycerol li
94	24	82.8	718	2	A82352	iron(III) compound
95	24	82.8	732	2	T43619	secreted protein k
96	24	82.8	732	2	S30060	protein kinase ypk
97	24	82.8	775	2	T40647	ubiquitin carboxyl
98	24	82.8	870	2	B40121	GTPase-activating
99	24	82.8	935	2	T51930	kinesin [imported]
100	24	82.8	942	2	JC7316	testicular zinc fi
101	24	82.8	1038	2	JT0663	ras GTPase-activat
102	24	82.8	1044	2	S01966	GTPase-activating
103	24	82.8	1047	2	A40121	GTPase-activating
104	24	82.8	1171	2	A37829	parasporal crystal
105	24	82.8	1171	2	I40572	parasporal crystal
106	24	82.8	1224	2	T14007	microtubule-associ
107	24	82.8	1242	2	S51246	probable DNA repai
108	24	82.8	1371	2	D82606	DNA primase XF2061
109	24	82.8	1374	2	T16129	hypothetical prote
110	24	82.8	1499	2	AC2555	hypothetical prote
111	24	82.8	1522	2	T39371	transcription regu
112	24	82.8	1634	2	T26517	hypothetical prote
113	24	82.8	1701	2	A26868	major merozoite su
114	24	82.8	1701	2	A54498	major merozoite su
115	24	82.8	2238	1	RRVUBY	genome polyprotein
116	24	82.8	2338	2	I73957	kinase-related pro
117	23	79.3	70	2	A59230	androgen-binding p
118	23	79.3	70	2	B59230	androgen-binding p
119	23	79.3	72	2	A46958	androgen-binding p
120	23	79.3	90	2	H83931	hypothetical prote
121	23	79.3	102	2	AE1099	B. subtilis SpoVG
122	23	79.3	104	1	WISMAT	alpha-amylase inhi
123	23	79.3	119	2	F65025	hypothetical prote
124	23	79.3	119	2	E91048	probable oxidoredu
125	23	79.3	119	2	A85893	probable oxidoredu
126	23	79.3	124	1	GCAF	glucagon 1 precurs
127	23	79.3	131	2	S63742	HIV-1 retropepsin
128	23	79.3	136	2	S63746	HIV-1 retropepsin
129	23	79.3	140	2	S63737	HIV-1 retropepsin
130	23	79.3	141	2	S63750	HIV-1 retropepsin

131	23	79.3	142	2	E72260	iron-sulfur cofact
132	23	79.3	146	2	E95363	protein [imported
133	23	79.3	151	2	S63748	HIV-1 retropepsin
134	23	79.3	151	2	S63731	HIV-1 retropepsin
135	23	79.3	162	2	S63732	HIV-1 retropepsin
136	23	79.3	196	2	AG2803	hypothetical prote
137	23	79.3	196	2	G97582	hypothetical prote
138	23	79.3	207	2	E64718	conserved hypothet
139	23	79.3	225	2	B84289	hypothetical prote
140	23	79.3	231	2	H64466	hypothetical prote
141	23	79.3	249	2	D85693	unknown protein en
142	23	79.3	260	2	E70578	probable wag31 pro
143	23	79.3	265	2	B96993	probable membrane
144	23	79.3	266	2	T26068	hypothetical prote
145	23	79.3	267	2	H97299	proB [imported] -
146	23	79.3	271	2	E84138	biotin synthesis B
147	23	79.3	274	2	T18768	hypothetical prote
148	23	79.3	275	2	D81947	probable amino aci
149	23	79.3	275	2	H81158	amino acid ABC tra
150	23	79.3	283	2	T05727	nucleic acid-bindin

ALIGNMENTS

RESULT 1

T19354

hypothetical protein C17E4.10 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004.

C;Accession: T19354

R;Percy, C.

submitted to the EMBL Data Library, October 1996 .

A;Reference number: Z19113

A;Accession: T19354

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-386

A;Cross-references: UNIPROT:Q93231; UNIPARC:UPI0000163FFD; EMBL:Z81037; PIDN:CAB02748.

A;Experimental source: clone C17E4

C;Genetics:

A;Gene: CESP:C17E4.10

A;Map position: 1

A;Introns: 36/3; 98/2; 264/3; 309/2

Query Match 96.6%; Score 28; DB 2; Length 386;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ADXTIXEE 8
 || || ||
 Db 134 ADTTIREE 141

RESULT 2

AI2108

hypothetical protein all2424 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AI2108

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-186.rnpbn.

[start](#)

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:17:32 ; Search time 55.6667 Seconds
(without alignments)
254.909 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+ _p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075109_19603/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10763712 @CGN_1_1_154 @runat_29062006_075109_19603 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Published_Applications_NA_New:*

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 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
c 1	28	96.6	3566	6	US-10-449-902-14853	Sequence 14853, A
c 2	28	96.6	3807	6	US-10-449-902-18976	Sequence 18976, A
c 3	28	96.6	6707	7	US-11-266-748A-32492	Sequence 32492, A
c 4	28	96.6	909203	7	US-11-266-748A-29039	Sequence 29039, A
c 5	27	93.1	369	7	US-11-266-748A-371617	Sequence 371617,
c 6	27	93.1	369	7	US-11-266-748A-454996	Sequence 454996,
7	27	93.1	675	7	US-11-217-529-5071	Sequence 5071, Ap
8	27	93.1	12783	7	US-11-266-748A-31917	Sequence 31917, A
9	27	93.1	13509	7	US-11-266-748A-29788	Sequence 29788, A
10	26	89.7	789	7	US-11-251-208-291	Sequence 291, App
11	26	89.7	1007	7	US-11-266-748A-254215	Sequence 254215,
12	26	89.7	1007	7	US-11-266-748A-276868	Sequence 276868,
c 13	26	89.7	1007	7	US-11-266-748A-314732	Sequence 314732,
14	26	89.7	1062	7	US-11-216-545-8455	Sequence 8455, Ap
15	26	89.7	1298	7	US-11-216-545-8456	Sequence 8456, Ap
16	26	89.7	3068	7	US-11-238-155-51	Sequence 51, Appl
17	26	89.7	3080	7	US-11-238-155-52	Sequence 52, Appl
18	26	89.7	3083	7	US-11-238-155-61	Sequence 61, Appl
19	26	89.7	3479	7	US-11-238-155-5	Sequence 5, Appli
20	26	89.7	12225	7	US-11-238-155-1	Sequence 1, Appli
21	25	86.2	520	6	US-10-488-619-2681	Sequence 2681, Ap
c 22	25	86.2	657	7	US-11-266-748A-80468	Sequence 80468, A
23	25	86.2	657	7	US-11-266-748A-133279	Sequence 133279,
c 24	25	86.2	1000	7	US-11-266-748A-209252	Sequence 209252,
c 25	25	86.2	1000	7	US-11-266-748A-223970	Sequence 223970,
26	25	86.2	1070	6	US-10-449-902-10908	Sequence 10908, A
c 27	25	86.2	1546	7	US-11-266-748A-57739	Sequence 57739, A
c 28	25	86.2	1918	7	US-11-266-748A-356895	Sequence 356895,
29	25	86.2	1918	7	US-11-266-748A-440274	Sequence 440274,
c 30	25	86.2	2391	6	US-10-449-902-27826	Sequence 27826, A
31	25	86.2	4614	7	US-11-257-817-33	Sequence 33, Appl
32	25	86.2	84323	7	US-11-266-748A-61233	Sequence 61233, A
33	24	82.8	306	7	US-11-301-554-1544	Sequence 1544, Ap
34	24	82.8	316	7	US-11-301-554-285	Sequence 285, App
c 35	24	82.8	438	7	US-11-266-748A-169643	Sequence 169643,
c 36	24	82.8	481	7	US-11-266-748A-5567	Sequence 5567, Ap
37	24	82.8	609	7	US-11-266-748A-299490	Sequence 299490,
c 38	24	82.8	614	6	US-10-488-619-2891	Sequence 2891, Ap
c 39	24	82.8	840	6	US-10-953-349-29706	Sequence 29706, A
c 40	24	82.8	1000	7	US-11-266-748A-215119	Sequence 215119,
c 41	24	82.8	1000	7	US-11-266-748A-216440	Sequence 216440,
42	24	82.8	1000	7	US-11-266-748A-238248	Sequence 238248,
c 43	24	82.8	1000	7	US-11-266-748A-283914	Sequence 283914,

	44	24	82.8	1000	7	US-11-266-748A-335343	Sequence 335343,
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	46	24	82.8	1018	7	US-11-266-748A-134840	Sequence 134840,
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c	48	24	82.8	1088	7	US-11-266-748A-369681	Sequence 369681,
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	51	24	82.8	1090	7	US-11-266-748A-436517	Sequence 436517,
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c	53	24	82.8	1133	7	US-11-266-748A-91013	Sequence 91013, A
	54	24	82.8	1133	7	US-11-266-748A-143824	Sequence 143824,
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	56	24	82.8	1201	6	US-10-953-349-4967	Sequence 4967, Ap
c	57	24	82.8	1373	7	US-11-266-748A-259201	Sequence 259201,
	58	24	82.8	1373	7	US-11-266-748A-319718	Sequence 319718,
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	60	24	82.8	1449	7	US-11-266-748A-149994	Sequence 149994,
	61	24	82.8	1464	7	US-11-266-748A-83761	Sequence 83761, A
c	62	24	82.8	1464	7	US-11-266-748A-136572	Sequence 136572,
	63	24	82.8	1549	7	US-11-266-748A-348836	Sequence 348836,
	64	24	82.8	1549	7	US-11-266-748A-382037	Sequence 382037,
c	65	24	82.8	1549	7	US-11-266-748A-432215	Sequence 432215,
	66	24	82.8	1627	6	US-10-953-349-33667	Sequence 33667, A
c	67	24	82.8	1739	7	US-11-266-748A-44623	Sequence 44623, A
	68	24	82.8	1752	6	US-10-449-902-24099	Sequence 24099, A
c	69	24	82.8	1883	7	US-11-266-748A-26763	Sequence 26763, A
c	70	24	82.8	1888	6	US-10-473-173-92	Sequence 92, Appl
c	71	24	82.8	1953	7	US-11-266-748A-29112	Sequence 29112, A
c	72	24	82.8	1988	7	US-11-266-748A-25783	Sequence 25783, A
c	73	24	82.8	1988	7	US-11-266-748A-31139	Sequence 31139, A
	74	24	82.8	1994	6	US-10-449-902-8412	Sequence 8412, Ap
c	75	24	82.8	2009	7	US-11-266-748A-76989	Sequence 76989, A
	76	24	82.8	2009	7	US-11-266-748A-129800	Sequence 129800,
	77	24	82.8	2052	6	US-10-471-571A-3983	Sequence 3983, Ap
c	78	24	82.8	2189	7	US-11-266-748A-24277	Sequence 24277, A
	79	24	82.8	2298	7	US-11-266-748A-186226	Sequence 186226,
	80	24	82.8	2381	6	US-10-449-902-27476	Sequence 27476, A
	81	24	82.8	2556	6	US-10-449-902-27174	Sequence 27174, A
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	83	24	82.8	2673	6	US-10-449-902-25815	Sequence 25815, A
c	84	24	82.8	2719	6	US-10-449-902-12244	Sequence 12244, A
	85	24	82.8	3547	7	US-11-293-697-1122	Sequence 1122, Ap
	86	24	82.8	3729	7	US-11-217-529-79062	Sequence 79062, A
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ALIGNMENTS

RESULT 1

US-10-449-902-14853

; Sequence 14853, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rnpbm.

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(without alignments)
244.665 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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SUMMARIES

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	4	28	96.6	5323	8	US-10-302-172-726	Sequence 726, App
c	5	28	96.6	519599	10	US-10-737-082-73	Sequence 73, Appl
c	6	28	96.6	519599	10	US-10-765-790-73	Sequence 73, Appl
	7	28	96.6	608916	10	US-10-461-862-1	Sequence 1, Appli
	8	27	93.1	345	8	US-10-424-599-126892	Sequence 126892,
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	12	27	93.1	756	8	US-10-424-599-31447	Sequence 31447, A
	13	27	93.1	909	10	US-10-511-561-18	Sequence 18, Appl
	14	27	93.1	1048	7	US-10-271-181B-102	Sequence 102, App
	15	27	93.1	1107	9	US-10-411-910A-134	Sequence 134, App
	16	27	93.1	1107	9	US-10-411-910A-241	Sequence 241, App
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	18	27	93.1	1170	9	US-10-411-910A-120	Sequence 120, App
	19	27	93.1	1170	9	US-10-411-910A-227	Sequence 227, App
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	22	27	93.1	1233	9	US-10-411-910A-174	Sequence 174, App
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39	27	93.1	1377	9	US-10-411-910A-228	Sequence 228, App
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ALIGNMENTS

RESULT 1

US-11-097-143-6821

; Sequence 6821, Application US/11097143

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rni.

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Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-186.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:00:56 ; Search time 73 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
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SUMMARIES

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5	27	93.1	2636	3	US-10-077-699C-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1

US-09-799-451-726

; Sequence 726, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

SCORE Search Results Details for Application 10 and Search Result us-10-763-712b-186.rn

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OM protein - nucleic search, using frame_plus_p2n model

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316.122 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	28	96.6	5264	10	ACC72807	Acc72807 Human can
	6	28	96.6	5323	12	ADM44362	Adm44362 Novel hum
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c	41	27	93.1	5172	10	ADB69592	Adb69592 C. neofor
	42	27	93.1	5200	14	ADY27766	Ady27766 Chlamydom
	43	27	93.1	5208	14	ADY27746	Ady27746 Chlamydom
c	44	27	93.1	6826	10	ADB69231	Adb69231 C. neofor
	45	27	93.1	12387	12	ADJ62733	Adj62733 Human cDN
	46	27	93.1	12780	2	AAX04535	Aax04535 DNA encod
	47	27	93.1	12780	8	ACC49402	Acc49402 Human DNA
	48	27	93.1	12783	10	ADD14669	Add14669 Human src
	49	27	93.1	13375	6	ABQ93457	Abq93457 Human cDN
	50	27	93.1	13468	6	ABQ93458	Abq93458 Human cDN
	51	27	93.1	13509	8	ABX76175	Abx76175 Lung canc
	52	27	93.1	13509	10	ADE85658	Ade85658 Farnesyl
	53	27	93.1	13509	10	ADF18734	Adf18734 DNA-depen
	54	27	93.1	13509	14	ADX05477	Adx05477 Cyclin-de
	55	27	93.1	13509	15	AEF74615	Aef74615 Human pol
	56	27	93.1	13509	15	AEF75056	Aef75056 Human pol
	57	26	89.7	30	3	AAZ97998	Aaz97998 HIV-1 pro
	58	26	89.7	51	6	ABA01273	Aba01273 Pseudokno
	59	26	89.7	54	3	AAA40249	Aaa40249 HIV-1 iso
c	60	26	89.7	84	2	AAV57198	Aav57198 Oligonucl
c	61	26	89.7	84	10	ADD54950	Add54950 Walk thro
	62	26	89.7	90	15	AEF88398	Aef88398 HIV-1 gag
	63	26	89.7	279	2	AAQ30211	Aaq30211 HIV-DASH
	64	26	89.7	297	2	AAQ34788	Aaq34788 Synthetic
	65	26	89.7	297	2	AAT67281	Aat67281 HIV-1 pro
	66	26	89.7	297	6	ABL39987	Abl39987 Synthetic
	67	26	89.7	297	6	ABL39988	Abl39988 Wild type
	68	26	89.7	297	6	ABL39985	Abl39985 Synthetic
	69	26	89.7	297	6	ABL39986	Abl39986 Wild type
	70	26	89.7	297	6	ABA01911	Aba01911 Human imm
	71	26	89.7	297	6	ABA01910	Aba01910 Human imm
	72	26	89.7	297	8	ACA03555	Aca03555 Synthetic
	73	26	89.7	297	8	ACA03556	Aca03556 Synthetic
	74	26	89.7	297	8	ACC78512	Acc78512 HIV protI
	75	26	89.7	297	8	ACC78511	Acc78511 HIV prot.
	76	26	89.7	297	10	ADC73264	Adc73264 NL4-3 Hum
	77	26	89.7	297	10	ADE29179	Ade29179 HIV-1 PR
	78	26	89.7	297	12	ADH56295	Adh56295 HIV NL4-3
	79	26	89.7	297	12	ADH67954	Adh67954 Human imm
	80	26	89.7	297	12	ADM73798	Adm73798 HIV-1 pol
	81	26	89.7	297	12	ADM73800	Adm73800 HIV-1 pol
	82	26	89.7	297	12	ADM73799	Adm73799 HIV-1 pol
	83	26	89.7	297	12	ADM73801	Adm73801 HIV-1 pol
	84	26	89.7	297	15	AEF07077	Aef07077 HIV-1 sub
	85	26	89.7	297	15	AEF07073	Aef07073 HIV-1 sub
	86	26	89.7	303	10	ADL18135	Adl18135 HIV-1 pro
	87	26	89.7	329	4	AAF28778	Aaf28778 HIV trans
	88	26	89.7	339	2	AAQ72414	Aaq72414 NY5 strai
	89	26	89.7	375	2	AAQ05116	Aaq05116 HIV-1 pro
	90	26	89.7	375	2	AAQ73660	Aaq73660 HIV-1 BH1
	91	26	89.7	402	2	AAQ05114	Aaq05114 HIV-1 pro
	92	26	89.7	477	1	AAN70427	Aan70427 The DNA s
	93	26	89.7	507	10	ADB87785	Adb87785 HIV-1 BH1
	94	26	89.7	507	10	ADD66307	Add66307 HIV-1 pro
	95	26	89.7	507	12	ADI05580	Adi05580 Novel ade
	96	26	89.7	507	13	ADS82142	Ads82142 DNA seque
	97	26	89.7	535	2	AAQ05115	Aaq05115 HIV-1 pro
	98	26	89.7	627	6	ABK78196	Abk78196 Bacillus
	99	26	89.7	630	2	AAQ11713	Aaq11713 Sequence
100	26	89.7	630	2	AAQ50157	Aaq50157 Gag and p	
101	26	89.7	660	2	AAZ21351	Aaz21351 Recombina	

102	26	89.7	751	6	ABK73718	Abk73718 Bacillus
103	26	89.7	789	13	ADT87706	Adt87706 Plant cDN
c 104	26	89.7	798	13	ADS58725	Ads58725 Bacterial
105	26	89.7	885	8	ACA22181	Aca22181 Prokaryot
106	26	89.7	898	8	ACA22453	Aca22453 Prokaryot
107	26	89.7	1009	11	ACN90366	Acn90366 Breast ca
c 108	26	89.7	1040	5	AAH80073	Aah80073 HIV PRT a
c 109	26	89.7	1040	10	ADD80964	Add80964 HIV PRT a
c 110	26	89.7	1040	14	ADW99666	Adw99666 HIV PRT D
111	26	89.7	1045	5	AAH51832	Aah51832 HIV prote
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114	26	89.7	1046	12	ADH44698	Adh44698 HIV prote
115	26	89.7	1053	5	AAH51871	Aah51871 HIV prote
116	26	89.7	1053	12	ADH44736	Adh44736 HIV prote
117	26	89.7	1059	5	AAH51870	Aah51870 HIV prote
118	26	89.7	1059	12	ADH44735	Adh44735 HIV prote
119	26	89.7	1082	5	AAH51872	Aah51872 HIV prote
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122	26	89.7	1113	12	ADH44721	Adh44721 HIV prote
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125	26	89.7	1115	5	AAH51927	Aah51927 HIV prote
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128	26	89.7	1115	12	ADH44792	Adh44792 HIV prote
129	26	89.7	1116	5	AAH51843	Aah51843 HIV prote
130	26	89.7	1116	5	AAH51873	Aah51873 HIV prote
131	26	89.7	1116	5	AAH51880	Aah51880 HIV prote
132	26	89.7	1116	5	AAH51944	Aah51944 HIV prote
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135	26	89.7	1116	5	AAH51932	Aah51932 HIV prote
136	26	89.7	1116	5	AAH51939	Aah51939 HIV prote
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138	26	89.7	1116	5	AAH51865	Aah51865 HIV prote
139	26	89.7	1116	5	AAH51878	Aah51878 HIV prote
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142	26	89.7	1116	5	AAH51914	Aah51914 HIV prote
143	26	89.7	1116	5	AAH51915	Aah51915 HIV prote
144	26	89.7	1116	5	AAH51924	Aah51924 HIV prote
145	26	89.7	1116	5	AAH51942	Aah51942 HIV prote
146	26	89.7	1116	5	AAH51884	Aah51884 HIV prote
147	26	89.7	1116	5	AAH51891	Aah51891 HIV prote
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ALIGNMENTS

RESULT 1

ABL06387

ID ABL06387 standard; cDNA; 1619 BP.

XX

AC ABL06387;

XX

DT 26-MAR-2002 (first entry)

XX

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b- 186.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:32:53 ; Search time 8 Seconds
(without alignments)
23.620 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA New:*

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match Length	DB	ID	Description
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2	25	86.2	205	6	US-10-449-902-39360
3	24	82.8	213	6	US-10-953-349-4970
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8	24	82.8	687	6	US-10-449-902-55507
9	23	79.3	124	6	US-10-953-349-25565
10	23	79.3	153	6	US-10-953-349-25564
11	23	79.3	177	6	US-10-449-902-35915
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18	23	79.3	283	6	US-10-953-349-21726
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25	23	79.3	358	6	US-10-449-902-47148
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64	22	75.9	509	6	US-10-449-902-32749	Sequence 32749, A
65	22	75.9	520	6	US-10-449-902-44765	Sequence 44765, A
66	22	75.9	521	6	US-10-449-902-40577	Sequence 40577, A
67	22	75.9	572	6	US-10-449-902-45447	Sequence 45447, A
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77	22	75.9	901	6	US-10-531-659-17	Sequence 17, Appl
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136	21	72.4	402	6	US-10-953-349-22470	Sequence 22470, A
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140	21	72.4	432	6	US-10-511-937-3004	Sequence 3004, Ap
141	21	72.4	437	6	US-10-449-902-32383	Sequence 32383, A
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147	21	72.4	485	6	US-10-953-349-36036	Sequence 36036, A
148	21	72.4	513	6	US-10-449-902-35344	Sequence 35344, A
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ALIGNMENTS

RESULT 1

US-11-251-208-292

; Sequence 292, Application US/11251208

; Publication No. US20060137043A1

; GENERAL INFORMATION:

; APPLICANT: Puzio, Piotr

; APPLICANT: Chardonnens, Agnes

; APPLICANT: Shirley, Amber

; APPLICANT: Wang, Xi-Qing

; APPLICANT: Sarria-Millan, Rodrigo

; APPLICANT: Mckersie, Bryan

; APPLICANT: Chen, Ruoying

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTI

; TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED

; TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS

; FILE REFERENCE: 13311-00015-US

; CURRENT APPLICATION NUMBER: US/11/251,208

; CURRENT FILING DATE: 2005-10-14

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; PRIOR FILING DATE: 2003-08-01

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OM protein - protein search, using sw model

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Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

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; Sequence 34, Application US/10813977

; Publication No. US20050220796A1

; GENERAL INFORMATION:

; APPLICANT: Dynan, William

; APPLICANT: Takeda, Yoshihiko

; APPLICANT: Li, Shuyi

; TITLE OF INVENTION: Compositions and Methods for Modulating DNA Repair

; FILE REFERENCE: 791301-1010

; CURRENT APPLICATION NUMBER: US/10/813,977

; CURRENT FILING DATE: 2004-03-31

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: non-binding sequence

US-10-813-977-34

Query Match 93.1%; Score 27; DB 5; Length 25;

Best Local Similarity 62.5%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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95	24	82.8	375	2	US-09-710-000-8	Sequence 8, Appli
96	24	82.8	383	2	US-10-057-531A-5	Sequence 5, Appli
97	24	82.8	391	2	US-10-057-531A-7	Sequence 7, Appli
98	24	82.8	393	2	US-10-057-531A-3	Sequence 3, Appli
99	24	82.8	394	2	US-08-195-705-4	Sequence 4, Appli
100	24	82.8	394	2	US-09-500-376-3	Sequence 3, Appli
101	24	82.8	417	2	US-09-540-236-3277	Sequence 3277, Ap
102	24	82.8	431	2	US-10-057-531A-2	Sequence 2, Appli
103	24	82.8	454	2	US-09-902-540-13578	Sequence 13578, A
104	24	82.8	485	2	US-10-130-419-1	Sequence 1, Appli
105	24	82.8	516	2	US-08-379-580-4	Sequence 4, Appli
106	24	82.8	519	2	US-09-252-991A-28349	Sequence 28349, A
107	24	82.8	546	2	US-10-057-531A-1	Sequence 1, Appli
108	24	82.8	616	2	US-09-248-796A-14992	Sequence 14992, A
109	24	82.8	669	2	US-09-617-594A-2	Sequence 2, Appli
110	24	82.8	669	2	US-10-209-507-2	Sequence 2, Appli
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112	24	82.8	720	2	US-09-902-540-13719	Sequence 13719, A
113	24	82.8	727	2	US-09-710-279-2862	Sequence 2862, Ap
114	24	82.8	738	2	US-09-134-001C-4285	Sequence 4285, Ap
115	24	82.8	870	1	US-08-190-687B-25	Sequence 25, Appl
116	24	82.8	870	5	PCT-US94-00198-5	Sequence 5, Appli
117	24	82.8	910	2	US-09-134-000C-4677	Sequence 4677, Ap
118	24	82.8	919	2	US-09-248-796A-18971	Sequence 18971, A
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121	24	82.8	1047	1	US-08-190-687B-8	Sequence 8, Appli

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139	23	79.3	91	2	US-09-621-976-5764	Sequence 5764, Ap
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143	23	79.3	160	2	US-09-605-703B-1532	Sequence 1532, Ap
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145	23	79.3	180	2	US-09-270-767-41783	Sequence 41783, A
146	23	79.3	188	2	US-09-621-976-5325	Sequence 5325, Ap
147	23	79.3	193	2	US-09-949-016-10446	Sequence 10446, A
148	23	79.3	213	2	US-09-540-236-2323	Sequence 2323, Ap
149	23	79.3	216	2	US-09-152-060-94	Sequence 94, Appl
150	23	79.3	216	2	US-09-852-797-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1

US-10-077-699C-6

; Sequence 6, Application US/10077699C

; Patent No. 6858718

; GENERAL INFORMATION:

; APPLICANT: Happe, Thomas

; TITLE OF INVENTION: Hydrogen Production

; FILE REFERENCE: 01MEL1

; CURRENT APPLICATION NUMBER: US/10/077,699C

; CURRENT FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Chlorella fusca

US-10-077-699C-6

Query Match 93.1%; Score 27; DB 2; Length 436;

Best Local Similarity 75.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ADXTIXEE 8

|| || ||

Db 105 ADLTIMEE 112

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b- 186.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:18:54 ; Search time 92.6667 Seconds
(without alignments)
39.472 Million cell updates/sec

Title: US-10-763-712B-186
Perfect score: 29
Sequence: 1 ADXTIXEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	96.6	1497	5	ABP69627	Abp69627 Human pol
3	27	93.1	8	9	AEB73400	Aeb73400 Segment o
4	27	93.1	25	9	AED26791	Aed26791 Control p
5	27	93.1	59	8	ADT91307	Adt91307 Clostridi
6	27	93.1	59	8	ADT91310	Adt91310 Chlamydom
7	27	93.1	303	7	ADF18725	Adf18725 DNA-depen
8	27	93.1	349	4	AAG81080	Aag81080 HIV prote
9	27	93.1	369	9	AEB73259	Aeb73259 Segment o
10	27	93.1	369	9	AEB73320	Aeb73320 Segment o
11	27	93.1	374	8	ADU00343	Adu00343 CpI catal
12	27	93.1	386	8	ADU00341	Adu00341 Iron hydr
13	27	93.1	388	7	ADF18726	Adf18726 DNA-depen
14	27	93.1	388	8	ADU00342	Adu00342 Iron hydr
15	27	93.1	389	9	AEB73245	Aeb73245 Segment o
16	27	93.1	393	8	ADU00340	Adu00340 Iron hydr
17	27	93.1	403	9	AEB73241	Aeb73241 Segment o
18	27	93.1	410	9	AEB73299	Aeb73299 Segment o
19	27	93.1	415	9	AEB73239	Aeb73239 Segment o
20	27	93.1	436	9	ADY27750	Ady27750 Chlorella
21	27	93.1	436	9	AEB73219	Aeb73219 Segment o
22	27	93.1	439	9	AEB73253	Aeb73253 Segment o
23	27	93.1	448	9	ADY27748	Ady27748 Scenedesm
24	27	93.1	449	9	AEB73297	Aeb73297 Segment o
25	27	93.1	449	9	AEB73318	Aeb73318 Segment o
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27	27	93.1	456	9	AEB73258	Aeb73258 Segment o
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37	27	93.1	505	9	AEB73240	Aeb73240 Segment o
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41	27	93.1	572	9	AEB73251	Aeb73251 Segment o
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55	27	93.1	582	7	ADC59546	Adc59546 Clostridi
56	27	93.1	582	8	ADR90318	Adr90318 Clostridi
57	27	93.1	582	9	AEB73237	Aeb73237 Segment o

58	27	93.1	582	9	AEB73315	Aeb73315	Segment o
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61	27	93.1	588	9	AEB73309	Aeb73309	Segment o
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64	27	93.1	608	9	AEB73304	Aeb73304	Segment o
65	27	93.1	636	9	AEB73243	Aeb73243	Segment o
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67	27	93.1	644	9	AEB73250	Aeb73250	Segment o
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79	27	93.1	4097	7	ADD14074	Add14074	Human src
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81	27	93.1	4128	5	ABP62979	Abp62979	Human pol
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83	27	93.1	4128	6	ABU03907	Abu03907	Human exp
84	27	93.1	4128	6	ABU03902	Abu03902	Human exp
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88	27	93.1	4128	9	ADX05478	Adx05478	Cyclin-de
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90	26	89.7	10	4	ABP18128	Abp18128	HIV B58 s
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92	26	89.7	10	4	ABP13546	Abp13546	HIV A02 s
93	26	89.7	15	9	ADV22394	Adv22394	HIV-1 Pol
94	26	89.7	15	9	ADV22393	Adv22393	HIV-1 Pol
95	26	89.7	17	9	ADV23802	Adv23802	HIV-1 pro
96	26	89.7	23	6	ABR55514	Abr55514	Amino aci
97	26	89.7	23	6	ABR55515	Abr55515	Protein p
98	26	89.7	36	5	AAU11473	Aau11473	Orthogona
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100	26	89.7	40	2	AAW04519	Aaw04519	HIV-1 K41
101	26	89.7	40	2	AAW04517	Aaw04517	HIV-1 K41
102	26	89.7	99	1	AAP81511	Aap81511	HIV-1 pro
103	26	89.7	99	2	AAR25641	Aar25641	HIV-1 AP
104	26	89.7	99	2	AAW04521	Aaw04521	HIV-1 K41
105	26	89.7	99	2	AAW30563	Aaw30563	HIV-1 GAG
106	26	89.7	99	2	AAW30570	Aaw30570	HIV-1 gag
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110	26	89.7	99	2	AAU77768	Aau77768	Human imm
111	26	89.7	99	2	AAU77769	Aau77769	Human imm
112	26	89.7	99	2	AAU77770	Aau77770	Human imm
113	26	89.7	99	2	AAU77772	Aau77772	Human imm
114	26	89.7	99	2	AAU77767	Aau77767	Human imm
115	26	89.7	99	2	AAU77771	Aau77771	Human imm
116	26	89.7	99	4	AAB37117	Aab37117	HIV trans
117	26	89.7	99	5	AAU11489	Aau11489	HIV prote
118	26	89.7	99	5	AAM51911	Aam51911	Human imm

119	26	89.7	99	5	AAM51912	Aam51912 Human imm
120	26	89.7	99	7	ADC73263	Adc73263 NL4-3 Hum
121	26	89.7	99	7	ADE29024	Ade29024 HIV-1 PR
122	26	89.7	99	7	ADE77498	Ade77498 Protease
123	26	89.7	99	7	ADE77511	Ade77511 Protease
124	26	89.7	99	7	ADE77502	Ade77502 Protease
125	26	89.7	99	7	ADE77519	Ade77519 Protease
126	26	89.7	99	7	ADE77560	Ade77560 Protease
127	26	89.7	99	7	ADE77497	Ade77497 Protease
128	26	89.7	99	7	ADE77499	Ade77499 Protease
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130	26	89.7	99	7	ADE77526	Ade77526 Protease
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134	26	89.7	99	7	ADE77558	Ade77558 Protease
135	26	89.7	99	7	ADE77527	Ade77527 Protease
136	26	89.7	99	7	ADE77506	Ade77506 Protease
137	26	89.7	99	7	ADE77513	Ade77513 Protease
138	26	89.7	99	7	ADE77524	Ade77524 Protease
139	26	89.7	99	7	ADE77559	Ade77559 Protease
140	26	89.7	99	7	ADE77503	Ade77503 Protease
141	26	89.7	99	7	ADE77518	Ade77518 Protease
142	26	89.7	99	7	ADE77525	Ade77525 Protease
143	26	89.7	99	7	ADE77512	Ade77512 Protease
144	26	89.7	99	7	ADE77528	Ade77528 Protease
145	26	89.7	99	7	ADE77496	Ade77496 Protease
146	26	89.7	99	7	ADE77505	Ade77505 Protease
147	26	89.7	99	7	ADE77520	Ade77520 Protease
148	26	89.7	99	7	ADE77501	Ade77501 Protease
149	26	89.7	99	7	ADE77545	Ade77545 Protease
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ALIGNMENTS

RESULT 1

ABR58656

ID ABR58656 standard; protein; 1482 AA.

XX

AC ABR58656;

XX

DT 09-JUL-2003 (first entry)

XX

DE Human cancer related protein SEQ ID NO:313.

XX

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

KW heart disease; atherosclerosis; endometriosis.

XX

OS Homo sapiens.

XX

PN WO2003025138-A2.

XX

PD 27-MAR-2003.

XX

PF 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rup.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:19:13 ; Search time 262.667 Seconds
(without alignments)
56.346 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	44	97.8	417	2	Q3MXY8_9DELT	Q3mxy8 syntrophoba
3	43	95.6	182	2	Q68YU4_9CLOT	Q68yu4 uncultured
4	43	95.6	182	2	Q68YV0_9CLOT	Q68yv0 uncultured

5	43	95.6	182	2	Q68YV1_9CLOT	Q68yv1 uncultured
6	43	95.6	183	2	Q68YU6_9CLOT	Q68yu6 uncultured
7	43	95.6	183	2	Q68YU7_9CLOT	Q68yu7 uncultured
8	43	95.6	218	2	Q2PWI4_9BACT	Q2pwi4 uncultured
9	43	95.6	218	2	Q2PWI5_9BACT	Q2pwi5 uncultured
10	43	95.6	218	2	Q2PWI9_9BACT	Q2pwi9 uncultured
11	43	95.6	219	2	Q2PWI6_9BACT	Q2pwi6 uncultured
12	43	95.6	219	2	Q38IH9_9BACT	Q38ih9 uncultured
13	43	95.6	221	2	Q2PWI1_9BACT	Q2pwi1 uncultured
14	43	95.6	221	2	Q2PWI3_9BACT	Q2pwi3 uncultured
15	43	95.6	221	2	Q38IH5_9BACT	Q38ih5 uncultured
16	43	95.6	221	2	Q38IH6_9BACT	Q38ih6 uncultured
17	43	95.6	221	2	Q38II2_9BACT	Q38ii2 uncultured
18	43	95.6	221	2	Q38II3_9BACT	Q38ii3 uncultured
19	43	95.6	221	2	Q38II5_9BACT	Q38ii5 uncultured
20	43	95.6	221	2	Q38II6_9BACT	Q38ii6 uncultured
21	43	95.6	221	2	Q38II8_9BACT	Q38ii8 uncultured
22	43	95.6	221	2	Q38IJ1_9BACT	Q38ij1 uncultured
23	43	95.6	221	2	Q38IJ3_9BACT	Q38ij3 uncultured
24	43	95.6	222	2	Q38II1_9BACT	Q38ii1 uncultured
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26	43	95.6	232	2	Q5Y8D3_9CLOT	Q5y8d3 clostridium
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28	43	95.6	387	2	Q3GDU8_9FIRM	Q3gdu8 syntrophomo
29	43	95.6	403	2	Q9AU60_SCEOB	Q9au60 scenedesmus
30	43	95.6	410	2	Q2Z381_9GAMM	Q2z381 shewanella
31	43	95.6	410	2	Q364V4_9GAMM	Q364v4 shewanella
32	43	95.6	410	2	Q8EAI2_SHEON	Q8eai2 shewanella
33	43	95.6	436	2	Q8VX03_CHLFU	Q8vx03 chlorella f
34	43	95.6	449	2	Q9AR66_SCEOB	Q9ar66 scenedesmus
35	43	95.6	456	2	Q67J76_SYMTH	Q67j76 symbiobacte
36	43	95.6	458	2	Q56UD8_CHLMO	Q56ud8 chlamydomon
37	43	95.6	471	2	Q6AR16_DESPS	Q6ar16 desulfotale
38	43	95.6	497	2	Q9FYU1_CHLRE	Q9fyu1 chlamydomon
39	43	95.6	505	2	Q6T532_CHLRE	Q6t532 chlamydomon
40	43	95.6	505	2	Q6T533_CHLRE	Q6t533 chlamydomon
41	43	95.6	505	2	Q8VZZ0_CHLRE	Q8vzz0 chlamydomon
42	43	95.6	527	2	Q426A0_DESHA	Q426a0 desulfitoba
43	43	95.6	563	2	Q3GAL4_9FIRM	Q3gal4 syntrophomo
44	43	95.6	572	2	Q9ZNE4_CLOPE	Q9zne4 clostridium
45	43	95.6	572	2	Q9RHU8_CLOPE	Q9rhu8 clostridium
46	43	95.6	573	2	Q2RHS0_MOOTH	Q2rhs0 moorella th
47	43	95.6	573	2	Q3ZA52_DEHE1	Q3za52 dehalococco
48	43	95.6	573	2	Q3ZWM9_DEHSC	Q3zwm9 dehalococco
49	43	95.6	574	1	PHF1_CLOPA	P29166 clostridium
50	43	95.6	574	2	Q3GAT5_9FIRM	Q3gat5 syntrophomo
51	43	95.6	574	2	Q3MXZ2_9DELT	Q3mxz2 syntrophoba
52	43	95.6	574	2	Q59261_CLOSA	Q59261 clostridium
53	43	95.6	578	2	Q93SF7_EUBAC	Q93sf7 eubacterium
54	43	95.6	579	2	Q2ZJ38_CALSA	Q2zj38 caldicellul
55	43	95.6	579	2	Q9XC55_CLOTM	Q9xc55 clostridium
56	43	95.6	581	2	Q3CJE2_THEET	Q3cje2 thermoanaer
57	43	95.6	581	2	Q8RBC8_THETN	Q8rbc8 thermoanaer
58	43	95.6	582	2	Q6F4C7_9CLOT	Q6f4c7 clostridium
59	43	95.6	582	2	Q4CDK8_CLOTM	Q4cdk8 clostridium
60	43	95.6	582	2	Q59262_CLOAB	Q59262 clostridium
61	43	95.6	588	2	Q8ABI6_BACTN	Q8abi6 bacteroides
62	43	95.6	591	2	Q3C5M2_9CLOT	Q3c5m2 alkaliphilu
63	43	95.6	596	2	Q67JF9_SYMTH	Q67jf9 symbiobacte
64	43	95.6	596	2	Q73MB6_TREDE	Q73mb6 treponema d
65	43	95.6	598	2	Q3A1L6_PELCD	Q3a1l6 pelobacter

66	43	95.6	605	2	Q2LSB7_9DELT	Q2lsb7 syntrophus
67	43	95.6	606	2	Q46606_DESVU	Q46606 desulfovibr
68	43	95.6	606	2	Q72B67_DESVH	Q72b67 desulfovibr
69	43	95.6	619	2	Q370P7_RHOPA	Q370p7 rhodopseudo
70	43	95.6	619	2	Q6NDH4_RHOPA	Q6ndh4 rhodopseudo
71	42	93.3	182	2	Q68YU8_9CLOT	Q68yu8 uncultured
72	42	93.3	220	2	Q2PWI7_9BACT	Q2pwi7 uncultured
73	42	93.3	220	2	Q2PWJ8_9BACT	Q2pwj8 uncultured
74	42	93.3	220	2	Q38II4_9BACT	Q38ii4 uncultured
75	42	93.3	230	2	Q38IH8_9BACT	Q38ih8 uncultured
76	42	93.3	389	2	Q86ZE7_NEOFR	Q86ze7 neocallimas
77	42	93.3	421	1	PHFL_DESVH	P07598 desulfovibr
78	42	93.3	421	1	PHFL_DESVO	P13629 desulfovibr
79	42	93.3	421	2	O08311_DESFR	O08311 desulfovibr
80	42	93.3	421	2	Q9AM36_DESDE	Q9am36 desulfovibr
81	42	93.3	421	2	Q317L4_DESDG	Q317l4 desulfovibr
82	42	93.3	439	2	Q30Z18_DESDG	Q30z18 desulfovibr
83	42	93.3	449	2	Q27096_TRIVA	Q27096 trichomonas
84	42	93.3	458	2	Q315X0_DESDG	Q315x0 desulfovibr
85	42	93.3	461	2	Q2WUD6_CLOBE	Q2wud6 clostridium
86	42	93.3	468	2	Q27094_TRIVA	Q27094 trichomonas
87	42	93.3	484	2	Q9RGN3_MEGEL	Q9rgn3 megasphaera
88	42	93.3	555	2	Q8TG63_9FUNG	Q8tg63 piromyces s
89	42	93.3	585	2	Q3A430_PELCD	Q3a430 pelobacter
90	42	93.3	608	2	Q9WY44_THEMA	Q9wy44 thermotoga
91	42	93.3	636	2	Q8TFP2_NEOFR	Q8tfp2 neocallimas
92	42	93.3	1198	2	Q5DM85_NYCOV	Q5dm85 nyctotherus
93	42	93.3	1206	2	O96948_NYCOV	O96948 nyctotherus
94	40	88.9	221	2	Q2PWI0_9BACT	Q2pwi0 uncultured
95	39	86.7	151	2	Q62AB0_BURMA	Q62ab0 burkholderi
96	39	86.7	156	2	Q5Y8C9_9CLOT	Q5y8c9 clostridium
97	39	86.7	156	2	Q68YU5_9CLOT	Q68yu5 uncultured
98	39	86.7	156	2	Q68YV3_9CLOT	Q68yv3 uncultured
99	39	86.7	156	2	Q68YV4_9CLOT	Q68yv4 uncultured
100	39	86.7	156	2	Q68YV5_9CLOT	Q68yv5 uncultured
101	39	86.7	170	2	Q63NP9_BURPS	Q63np9 burkholderi
102	39	86.7	171	2	Q3X5V2_9ACTN	Q3x5v2 rubrobacter
103	39	86.7	182	2	Q68YV2_9CLOT	Q68yv2 uncultured
104	39	86.7	186	2	Q4AWQ7_9BURK	Q4awq7 polaromonas
105	39	86.7	238	2	Q5Y8D0_9CLOT	Q5y8d0 clostridium
106	39	86.7	238	2	Q5Y8D1_9CLOT	Q5y8d1 clostridium
107	39	86.7	582	2	Q3C9E8_9CLOT	Q3c9e8 alkaliphilu
108	39	86.7	644	2	Q2WI78_CLOBE	Q2wi78 clostridium
109	38	84.4	585	2	Q3A458_PELCD	Q3a458 pelobacter
110	38	84.4	585	2	Q46508_DESFR	Q46508 desulfovibr
111	37	82.2	157	2	Q8TVJ9_METKA	Q8tvj9 methanopyru
112	37	82.2	159	2	Q3Z8W3_DEHE1	Q3z8w3 dehalococco
113	37	82.2	159	2	Q3ZX10_DEHSC	Q3zx10 dehalococco
114	37	82.2	644	2	Q4CDI0_CLOTM	Q4cdi0 clostridium
115	37	82.2	1150	2	Q420N6_DESHA	Q420n6 desulfitoba
116	36	80.0	154	2	Q3A2Y3_PELCD	Q3a2y3 pelobacter
117	36	80.0	169	2	Q8TMY5_METAC	Q8tmy5 methanosarc
118	35	77.8	104	2	Q2L9Z3_9CLOT	Q2l9z3 uncultured
119	35	77.8	104	2	Q2L9Z4_9CLOT	Q2l9z4 uncultured
120	35	77.8	104	2	Q2L9Z5_9CLOT	Q2l9z5 uncultured
121	35	77.8	104	2	Q2L9Z7_9CLOT	Q2l9z7 uncultured
122	35	77.8	104	2	Q2L9Z8_9CLOT	Q2l9z8 uncultured
123	35	77.8	104	2	Q2L9Z9_9CLOT	Q2l9z9 uncultured
124	35	77.8	104	2	Q2LA00_9CLOT	Q2la00 uncultured
125	35	77.8	175	2	Q40LF6_DESAC	Q40lf6 desulfuromo
126	35	77.8	380	1	T701_FREDI	Q00461 fremyella d

127	35	77.8	566	2	O83356_TREPA	O83356 treponema p
128	34	75.6	104	2	Q2L9Z6_9CLOT	Q2L9Z6 uncultured
129	34	75.6	152	2	Q33L36_METHU	Q33L36 methanospir
130	34	75.6	156	2	Q8PSK4_METMA	Q8psk4 methanosarc
131	34	75.6	176	2	Q469W1_METBA	Q469w1 methanosarc
132	34	75.6	375	2	Q8UKQ6_AGRT5	Q8ukq6 agrobacteri
133	34	75.6	388	2	Q7D419_AGRT5	Q7d419 agrobacteri
134	34	75.6	390	2	Q3ATR4_CHLCH	Q3atr4 chlorobium
135	34	75.6	440	2	Q5LTL3_SILPO	Q5ltl3 silicibacte
136	34	75.6	706	2	Q498X7_BRARE	Q498x7 brachydanio
137	34	75.6	706	2	Q8AW58_BRARE	Q8aw58 brachydanio
138	34	75.6	766	2	Q4DKD9_TRYCR	Q4dkd9 trypanosoma
139	34	75.6	766	2	Q4CVY5_TRYCR	Q4cvy5 trypanosoma
140	34	75.6	820	2	O45155_CAEEL	O45155 caenorhabdi
141	33	73.3	117	2	Q7XEE9_ORYSA	Q7xee9 oryza sativ
142	33	73.3	151	2	O29139_ARCFU	O29139 archaeoglob
143	33	73.3	153	2	Q3IU16_NATPD	Q3iu16 natronomona
144	33	73.3	165	2	Q3VXV2_9ACTO	Q3vxv2 fränkia sp.
145	33	73.3	170	2	Q3JHK8_BURP1	Q3jhk8 burkholderi
146	33	73.3	182	2	Q4BTU9_BURVI	Q4btu9 burkholderi
147	33	73.3	184	2	Q44WD0_9BURK	Q44wd0 burkholderi
148	33	73.3	184	2	Q4LQR6_9BURK	Q4lqr6 burkholderi
149	33	73.3	356	2	Q2JPT3_9CYAN	Q2jpt3 cyanobacter
150	33	73.3	356	2	Q2JW91_9CYAN	Q2jw91 cyanobacter

ALIGNMENTS

RESULT 1

Q9GTP2_TRIVA

ID Q9GTP2_TRIVA PRELIMINARY; PRT; 589 AA.
AC Q9GTP2;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Putative 64kDa iron hydrogenase (Fragment).
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
OC Trichomonadidae; Trichomonadinae; Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20523972; PubMed=11070057;
RA Horner D.S., Foster P.G., Embley M.T.;
RT "Iron hydrogenases and the evolution of anaerobic eukaryotes.";
RL Mol. Biol. Evol. 17:1695-1709(2000).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF262401; AAG31037.1; -; mRNA.
DR HSSP; P07598; 1HFE.
DR GO; GO:0042597; C:periplasmic space; IEA.
DR GO; GO:0051539; F:4 iron, 4 sulfur cluster binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0008901; F:ferredoxin hydrogenase activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.

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[start](#)

A;Cross-references: UNIPROT:O83356; UNIPARC:UPI00000D3239; GB:AE001213; GB:AE000520;
- Agrobacterium tumefaciens (strain C58, Dupont) plasmid AT C;Species: Agrobacterium tumefaciens
A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; K
PMID:11743193 A;Accession: AB3165 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-
FXXXGGVMEAAXR 16 || :||| | Db 173 FDTSGGYVEAAVR 185 RESULT 13 G88996 protein C17B7.5
PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Pr
C17B7.5 A;Map position: 5 Query Match 75.6%; Score 34; DB 2; Length 820; Best Local Similarity
O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richards
Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland
A;Cross-references: UNIPROT:O29139; UNIPARC:UPI0000056E45; GB:AE001026; GB:AE000782;
pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Acces
SPDB:SPCC285.11 A;Experimental source: strain 972h-; cosmid c285 C;Genetics: A;Gene: SPDB:5
#text_change 18-Feb-2000 C;Accession: D36144 R;Crouzet, J.; Cauchois, L.; Blanche, F.; Debuss
MUID:91008975; PMID:2211520 A;Accession: D36144 A;Status: preliminary A;Molecule type: DN
RESULT 17 JC4118 probable site-specific integrase - phage Cf1t N;Alternate names: ORF344 C;Spe
A;Accession: JC4118 A;Molecule type: DNA A;Residues: 1-344 A;Cross-references: UNIPROT:Q375
disease in orange. C;Genetics: A;Start codon: GTG C;Superfamily: phage Cf1t integrase C;Keywo
Xanthomonas campestris C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20
UNIPARC:UPI000009B339; GB:U38235; NID:g1185453; PIDN:AAC54630.1; PID:g1185454 A;Expe
53.8%; Pred. No. 34; Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0; Qy 4 FXXXGGV
F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbro
PMID:10984043 A;Accession: E83637 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2
66.7%; Pred. No. 40; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 8 GGVMEAA
R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V. Nature 392, 353-358, 1998 A;Title: The complete ge
GB:AE000657 A;Experimental source: strain VF5 C;Genetics: A;Gene: aq_1884 Query Match 68.9
C72672 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
Aeropyrum pernix K1. A;Reference number: A72450; MUID:99310339; PMID:10382966 A;Accessio
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Qy 8 GGVMEAAXR 16 || :||| | Db 138
Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand,
Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P. A;1
C;Superfamily: short protease IV-related protein Query Match 68.9%; Score 31; DB 2; Length 337
L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; C
A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Rammel, B.
PIDN:CAC96858.1; PID:g16414114; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;
(strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-9
I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;
PASP:PA1410 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA1410 C;Superfamily: spi
#sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: F87508 R;Nierman, W.C
Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141,
conserved probable membrane protein YIL003w Query Match 68.9%; Score 31; DB 2; Length 366;
C;Accession: A98315 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.
Agrobacterium tumefaciens C58. A;Reference number: A97359; MUID:21608551; PMID:11743194
Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 8 GGVMEAAXR 16 |||:| | Db 273 GGVVEASC
Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guer
Olson, M.V.; Nester, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tum
chromosome Query Match 68.9%; Score 31; DB 2; Length 377; Best Local Similarity 66.7%; Pred.

carboxyvinyltransferase (EC 2.5.1.19); shikimate 5-dehydrogenase (EC 1.1.1.25); shikimate kinase
 MUID:88076802; PMID:2825635 A;Accession: A32519 A;Molecule type: DNA A;Residues: 1-1588
 GSPDB:GN00004; MIPS:YDR127w R;Duncan, K.; Edwards, R.M.; Coggins, J.R. FEBS Lett. 241, 83-
 A;Gene: SGD:ARO1; MIPS:YDR127w A;Cross-references: SGD:S0002534; MIPS:YDR127w A;Map |
 phosphorus-oxygen lyase; phosphotransferase F;7-380/Domain: 3-dehydroquinase synthase homo
 Gaps 0; Qy 4 FXXXGGVMEAA 14 ||::|| Db 966 FSTGGGIVESA 976 RESULT 29 D97316 probable
 Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequ
 Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC3389 Query Match 68.9%; Score 31
 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004 C;Accession: AH2414
 Anabaena sp. strain PCC 7120. A;Reference number: AB1807; MUID:21595285; PMID:11759840 A
 40; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Qy 8 GGVMEAAAXR 16 ||::|| Db

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:24:08 ; Search time 31.3333 Seconds
 (without alignments)
 49.132 Million cell updates/sec

Title: US-10-763-712B-185
 Perfect score: 45
 Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : PIR_80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	43	95.6	574	1	HQCL1P	hydrogenase (EC 1.
2	43	95.6	582	2	D96903	hydrogene dehydrog
3	43	95.6	582	2	JC6002	hydrogenase (EC 1.
4	43	95.6	606	2	S13526	hydrogenase (EC 1.
5	42	93.3	421	1	HQDVFL	cytochrome-c3 hydr
6	42	93.3	421	1	HQDVLV	cytochrome-c3 hydr

7	42	93.3	608	2	C72405	hydrogenase (EC 1.
8	42	93.3	1206	2	T18557	probable hydrogenase
9	38	84.4	585	2	D57150	hydrogenase (EC 1.
10	35	77.8	380	2	S16891	probable transposase
11	35	77.8	566	2	F71337	probable comE protein
12	34	75.6	375	2	AB3165	conserved hypothetical
13	34	75.6	820	2	G88996	protein C17B7.5 [i
14	33	73.3	151	2	E69390	P450 cytochrome h
15	33	73.3	427	2	T41257	hypothetical prote
16	32	71.1	333	2	D36144	cobC protein - Pse
17	32	71.1	344	1	JC4118	probable site-spec
18	32	71.1	346	2	JC4582	replication initia
19	31	68.9	242	2	E83637	probable phosphopr
20	31	68.9	250	2	D70462	conserved hypothet
21	31	68.9	293	2	C72672	probable survival
22	31	68.9	337	2	AI1272	proteinase homolog
23	31	68.9	337	2	AB1636	proteinases homolo
24	31	68.9	363	2	A83470	probable periplasm
25	31	68.9	366	2	F87508	GTP-binding protei
26	31	68.9	377	2	A98315	hypothetical prote
27	31	68.9	377	2	AB2968	conserved hypothet
28	31	68.9	1588	1	BVBYA1	3-dehydroquinatase
29	31	68.9	1939	2	D97316	probable S-layer p
30	30	66.7	147	2	AH2414	hypothetical prote
31	30	66.7	230	2	E95017	ABC transporter, p
32	30	66.7	230	2	F97890	hypothetical prote
33	30	66.7	244	2	T39507	probable ATP synth
34	30	66.7	261	2	D98256	hypothetical prote
35	30	66.7	261	2	AG3028	hypothetical prote
36	30	66.7	274	2	F86264	proteasome endopep
37	30	66.7	306	2	F69129	tungsten formylmet
38	30	66.7	323	2	E86935	conserved hypothet
39	30	66.7	356	2	H82639	hypothetical prote
40	30	66.7	362	2	A49316	chorismate synthas
41	30	66.7	377	2	F69008	acetyltransferase
42	30	66.7	475	2	H84137	hypothetical prote
43	30	66.7	631	2	H70835	hypothetical prote
44	30	66.7	650	2	AE1992	ABC transporter AT
45	30	66.7	695	2	G64327	H+-transporting tw
46	30	66.7	839	2	F85334	myosin heavy chain
47	30	66.7	1101	2	G83637	hypothetical prote
48	30	66.7	1175	2	T20346	pyruvate carboxyla
49	30	66.7	1178	1	A47255	pyruvate carboxyla
50	30	66.7	1178	1	JC2460	pyruvate carboxyla
51	30	66.7	1178	2	JC4391	pyruvate carboxyla
52	30	66.7	1195	2	T43735	pyruvate carboxyla
53	30	66.7	1446	2	T04528	myosin heavy chain
54	30	66.7	1477	2	T00957	myosin heavy chain
55	30	66.7	1515	2	S51824	myosin heavy chain
56	30	66.7	1611	2	A84743	probable myosin he
57	30	66.7	1643	2	T07961	myosin heavy chain
58	30	66.7	1736	2	F86178	hypothetical prote
59	30	66.7	1738	2	C84507	hypothetical prote
60	29	64.4	175	2	H71249	hypothetical prote
61	29	64.4	181	2	AE0018	probable hydrolase
62	29	64.4	188	2	E75365	kanamycin resistan
63	29	64.4	228	2	D84261	hypothetical prote
64	29	64.4	260	2	G87349	conserved hypothet
65	29	64.4	320	2	JC7929	ATP-dependent gluc
66	29	64.4	376	2	F72514	probable glucokina
67	29	64.4	379	2	AI1391	UDP-N-acetylglucos

68	29	64.4	379	2	AC1767	UDP-N-acetylglucos
69	29	64.4	387	2	F82692	conserved hypothet
70	29	64.4	406	2	A69553	conserved hypothet
71	29	64.4	413	2	A95874	probable D-amino-a
72	29	64.4	433	1	S22284	transcription regu
73	29	64.4	500	2	T22068	hypothetical prote
74	29	64.4	507	2	AF0974	phosphoglycerate m
75	29	64.4	514	2	C86037	hypothetical prote
76	29	64.4	514	2	B91190	hypothetical prote
77	29	64.4	514	2	S47833	probable phosphogl
78	29	64.4	633	2	AD1116	internalin, probab
79	29	64.4	748	2	T47250	complex I intermed
80	29	64.4	750	2	E84475	probable Athila re
81	29	64.4	783	2	AG3402	polyphosphate kina
82	29	64.4	999	2	AG2413	hypothetical prote
83	29	64.4	1176	2	S66771	hypothetical prote
84	29	64.4	1677	2	T46095	hypothetical prote
85	29	64.4	2201	2	AH0095	probable sideropho
86	28	62.2	70	2	S25190	pilin precursor -
87	28	62.2	100	2	S72816	hypothetical prote
88	28	62.2	113	2	T30041	hypothetical prote
89	28	62.2	128	2	T28433	selenophosphate sy
90	28	62.2	152	2	S57421	cysteine proteinas
91	28	62.2	155	2	AD2801	bacterioferritin c
92	28	62.2	155	2	F97580	bacterioferritin c
93	28	62.2	166	2	I53166	leptin precursor -
94	28	62.2	167	1	LTHU	leptin precursor -
95	28	62.2	172	2	JE0392	inorganic diphosph
96	28	62.2	173	2	A70017	4-hydroxybenzoyl-C
97	28	62.2	181	2	S39717	ywdL protein - Bac
98	28	62.2	185	2	A64159	intracellular sept
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100	28	62.2	210	2	C81216	conserved hypothet
101	28	62.2	210	2	G81793	hypothetical prote
102	28	62.2	223	2	E75390	phage shock protei
103	28	62.2	264	2	E81127	hypothetical prote
104	28	62.2	264	2	H81834	hypothetical prote
105	28	62.2	268	2	AD2622	conserved hypothet
106	28	62.2	276	2	AE3543	3-isopropylmalate
107	28	62.2	285	2	A84224	cytochrome c oxida
108	28	62.2	293	2	E83749	glucose kinase BH0
109	28	62.2	296	2	A95276	probable KduI DKI
110	28	62.2	306	2	D97404	probable dapE gene
111	28	62.2	323	2	B70561	probable mesJ prot
112	28	62.2	325	2	I57009	3-Hydroxy-3-methyl
113	28	62.2	331	2	F84049	proteinase IV BH31
114	28	62.2	334	2	C87508	HlyD family secret
115	28	62.2	336	2	AD0781	galactoside transp
116	28	62.2	336	2	B85853	hypothetical prote
117	28	62.2	336	2	C37277	transmembrane pore
118	28	62.2	336	2	H91008	hypothetical prote
119	28	62.2	336	2	I64096	transmembrane pore
120	28	62.2	336	2	AI0183	galactoside permea
121	28	62.2	337	2	F82214	galactoside ABC tr
122	28	62.2	348	2	T51781	protein kinase AtPP
123	28	62.2	349	2	D70543	probable nadA prot
124	28	62.2	352	2	C84199	hypothetical prote
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127	28	62.2	357	2	A23641	RP2 protein, testo
128	28	62.2	362	1	S12581	cysteine proteinas

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:17:32 ; Search time 111.333 Seconds
(without alignments)
254.909 Million cell updates/sec

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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	35	77.8	974	6	US-10-449-902-15171			Sequence 15171, A
c	3	35	77.8	1435	6	US-10-449-902-7815			Sequence 7815, Ap
c	4	35	77.8	1497	6	US-10-449-902-21825			Sequence 21825, A
c	5	35	77.8	1516	6	US-10-449-902-20898			Sequence 20898, A
c	6	34	75.6	1628	6	US-10-449-902-14499			Sequence 14499, A
c	7	34	75.6	1628	6	US-10-449-902-21751			Sequence 21751, A
c	8	33	73.3	907	7	US-11-266-748A-480315			Sequence 480315,
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c	10	33	73.3	926	7	US-11-266-748A-86752			Sequence 86752, A
	11	33	73.3	926	7	US-11-266-748A-139563			Sequence 139563,
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c 115	31	68.9	13042	7	US-11-236-836-17	Sequence 17, Appl
c 116	31	68.9	13042	7	US-11-236-836-23	Sequence 23, Appl
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ALIGNMENTS

RESULT 1

US-10-449-902-12209/c

; Sequence 12209, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

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(without alignments)
244.665 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+ _p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075105_19496/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=150 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10763712 @CGN_1_1_2326 @runat_29062006_075105_19496 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Published_Applications_NA_Main:*

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	1770	9	US-10-411-910A-110	Sequence 110, App
2	45	100.0	1770	9	US-10-411-910A-217	Sequence 217, App
3	44	97.8	39	9	US-10-411-910A-287	Sequence 287, App
4	44	97.8	39	9	US-10-411-910A-299	Sequence 299, App
5	44	97.8	39	9	US-10-411-910A-313	Sequence 313, App
6	44	97.8	39	9	US-10-411-910A-319	Sequence 319, App
7	44	97.8	39	9	US-10-411-910A-323	Sequence 323, App
8	43	95.6	39	9	US-10-411-910A-301	Sequence 301, App
9	43	95.6	39	9	US-10-411-910A-305	Sequence 305, App
10	43	95.6	39	9	US-10-411-910A-315	Sequence 315, App
11	43	95.6	39	9	US-10-411-910A-317	Sequence 317, App
12	43	95.6	39	9	US-10-411-910A-321	Sequence 321, App
13	43	95.6	39	9	US-10-411-910A-325	Sequence 325, App
14	43	95.6	39	9	US-10-411-910A-327	Sequence 327, App
15	43	95.6	39	9	US-10-411-910A-329	Sequence 329, App
16	43	95.6	1212	9	US-10-411-910A-115	Sequence 115, App
17	43	95.6	1212	9	US-10-411-910A-222	Sequence 222, App
18	43	95.6	1233	9	US-10-411-910A-174	Sequence 174, App
19	43	95.6	1233	9	US-10-411-910A-281	Sequence 281, App
20	43	95.6	1248	9	US-10-411-910A-113	Sequence 113, App
21	43	95.6	1248	9	US-10-411-910A-220	Sequence 220, App
22	43	95.6	1311	9	US-10-411-910A-93	Sequence 93, Appl
23	43	95.6	1311	9	US-10-411-910A-200	Sequence 200, App
24	43	95.6	1311	10	US-10-763-712A-178	Sequence 178, App
25	43	95.6	1350	9	US-10-411-910A-92	Sequence 92, Appl
26	43	95.6	1350	9	US-10-411-910A-199	Sequence 199, App
27	43	95.6	1350	10	US-10-763-712A-177	Sequence 177, App
28	43	95.6	1494	9	US-10-411-910A-112	Sequence 112, App
29	43	95.6	1494	9	US-10-411-910A-219	Sequence 219, App
30	43	95.6	1494	10	US-10-763-712A-173	Sequence 173, App
31	43	95.6	1518	9	US-10-411-910A-114	Sequence 114, App
32	43	95.6	1518	9	US-10-411-910A-221	Sequence 221, App
33	43	95.6	1665	9	US-10-411-910A-122	Sequence 122, App
34	43	95.6	1665	9	US-10-411-910A-229	Sequence 229, App
35	43	95.6	1719	9	US-10-411-910A-98	Sequence 98, Appl

36	43	95.6	1719	9	US-10-411-910A-99	Sequence 99, Appl
37	43	95.6	1719	9	US-10-411-910A-126	Sequence 126, App
38	43	95.6	1719	9	US-10-411-910A-205	Sequence 205, App
39	43	95.6	1719	9	US-10-411-910A-206	Sequence 206, App
40	43	95.6	1719	9	US-10-411-910A-233	Sequence 233, App
41	43	95.6	1725	9	US-10-411-910A-89	Sequence 89, Appl
42	43	95.6	1725	9	US-10-411-910A-94	Sequence 94, Appl
43	43	95.6	1725	9	US-10-411-910A-196	Sequence 196, App
44	43	95.6	1725	9	US-10-411-910A-201	Sequence 201, App
45	43	95.6	1725	10	US-10-763-712A-174	Sequence 174, App
46	43	95.6	1737	9	US-10-411-910A-123	Sequence 123, App
47	43	95.6	1737	9	US-10-411-910A-230	Sequence 230, App
48	43	95.6	1740	8	US-10-282-122A-16510	Sequence 16510, A
49	43	95.6	1746	9	US-10-411-910A-116	Sequence 116, App
50	43	95.6	1746	9	US-10-411-910A-223	Sequence 223, App
51	43	95.6	1749	8	US-10-282-122A-15841	Sequence 15841, A
52	43	95.6	1749	9	US-10-411-910A-111	Sequence 111, App
53	43	95.6	1749	9	US-10-411-910A-218	Sequence 218, App
54	43	95.6	1821	9	US-10-411-910A-97	Sequence 97, Appl
55	43	95.6	1821	9	US-10-411-910A-117	Sequence 117, App
56	43	95.6	1821	9	US-10-411-910A-204	Sequence 204, App
57	43	95.6	1821	9	US-10-411-910A-224	Sequence 224, App
58	43	95.6	1860	9	US-10-411-910A-124	Sequence 124, App
59	43	95.6	1860	9	US-10-411-910A-231	Sequence 231, App
60	43	95.6	2399	16	US-11-015-540-8	Sequence 8, Appli
61	43	95.6	2421	16	US-11-015-540-9	Sequence 9, Appli
62	43	95.6	2636	16	US-11-015-540-7	Sequence 7, Appli
63	43	95.6	3265	16	US-11-015-540-3	Sequence 3, Appli
64	43	95.6	5001	16	US-11-015-540-1	Sequence 1, Appli
65	43	95.6	5208	16	US-11-015-540-2	Sequence 2, Appli
66	42	93.3	39	9	US-10-411-910A-283	Sequence 283, App
67	42	93.3	39	9	US-10-411-910A-285	Sequence 285, App
68	42	93.3	39	9	US-10-411-910A-291	Sequence 291, App
69	42	93.3	39	9	US-10-411-910A-293	Sequence 293, App
70	42	93.3	39	9	US-10-411-910A-295	Sequence 295, App
71	42	93.3	39	9	US-10-411-910A-297	Sequence 297, App
72	42	93.3	39	9	US-10-411-910A-303	Sequence 303, App
73	42	93.3	39	9	US-10-411-910A-307	Sequence 307, App
74	42	93.3	39	9	US-10-411-910A-309	Sequence 309, App
75	42	93.3	1137	9	US-10-411-910A-129	Sequence 129, App
76	42	93.3	1137	9	US-10-411-910A-236	Sequence 236, App
77	42	93.3	1170	9	US-10-411-910A-120	Sequence 120, App
78	42	93.3	1170	9	US-10-411-910A-227	Sequence 227, App
79	42	93.3	1265	10	US-10-763-712A-175	Sequence 175, App
80	42	93.3	1266	9	US-10-411-910A-90	Sequence 90, Appl
81	42	93.3	1266	9	US-10-411-910A-95	Sequence 95, Appl
82	42	93.3	1266	9	US-10-411-910A-101	Sequence 101, App
83	42	93.3	1266	9	US-10-411-910A-103	Sequence 103, App
84	42	93.3	1266	9	US-10-411-910A-130	Sequence 130, App
85	42	93.3	1266	9	US-10-411-910A-197	Sequence 197, App
86	42	93.3	1266	9	US-10-411-910A-202	Sequence 202, App
87	42	93.3	1266	9	US-10-411-910A-208	Sequence 208, App
88	42	93.3	1266	9	US-10-411-910A-210	Sequence 210, App
89	42	93.3	1266	9	US-10-411-910A-237	Sequence 237, App
90	42	93.3	1320	9	US-10-411-910A-128	Sequence 128, App
91	42	93.3	1320	9	US-10-411-910A-235	Sequence 235, App
92	42	93.3	1350	9	US-10-411-910A-109	Sequence 109, App
93	42	93.3	1350	9	US-10-411-910A-216	Sequence 216, App
94	42	93.3	1377	9	US-10-411-910A-121	Sequence 121, App
95	42	93.3	1377	9	US-10-411-910A-228	Sequence 228, App
96	42	93.3	1407	9	US-10-411-910A-108	Sequence 108, App

97	42	93.3	1407	9	US-10-411-910A-215	Sequence 215, App
98	42	93.3	1455	9	US-10-411-910A-100	Sequence 100, App
99	42	93.3	1455	9	US-10-411-910A-207	Sequence 207, App
100	42	93.3	1668	9	US-10-411-910A-119	Sequence 119, App
101	42	93.3	1668	9	US-10-411-910A-226	Sequence 226, App
102	42	93.3	1827	9	US-10-411-910A-104	Sequence 104, App
103	42	93.3	1827	9	US-10-411-910A-211	Sequence 211, App
104	42	93.3	1911	9	US-10-411-910A-118	Sequence 118, App
105	42	93.3	1911	9	US-10-411-910A-225	Sequence 225, App
106	42	93.3	3621	9	US-10-411-910A-106	Sequence 106, App
107	42	93.3	3621	9	US-10-411-910A-213	Sequence 213, App
108	38	84.4	38	9	US-10-411-910A-289	Sequence 289, App
109	38	84.4	38	9	US-10-411-910A-311	Sequence 311, App
110	38	84.4	1758	9	US-10-411-910A-102	Sequence 102, App
111	38	84.4	1758	9	US-10-411-910A-209	Sequence 209, App
c 112	37	82.2	643	4	US-09-925-065A-855143	Sequence 855143,
c 113	37	82.2	643	5	US-09-925-065A-855143	Sequence 855143,
c 114	37	82.2	663	4	US-09-925-065A-852012	Sequence 852012,
c 115	37	82.2	663	5	US-09-925-065A-852012	Sequence 852012,
116	37	82.2	1935	9	US-10-411-910A-125	Sequence 125, App
117	37	82.2	1935	9	US-10-411-910A-232	Sequence 232, App
c 118	37	82.2	1694969	12	US-10-506-454-1690	Sequence 1690, Ap
c 119	36	80.0	1777	8	US-10-437-963-62301	Sequence 62301, A
c 120	36	80.0	3797	13	US-11-097-143-32713	Sequence 32713, A
c 121	35	77.8	592	8	US-10-424-599-81874	Sequence 81874, A
c 122	35	77.8	992	8	US-10-437-963-11247	Sequence 11247, A
c 123	35	77.8	1481	8	US-10-425-114-21175	Sequence 21175, A
124	35	77.8	1552	10	US-10-499-353A-252	Sequence 252, App
c 125	35	77.8	1631	9	US-10-425-115-136309	Sequence 136309,
126	35	77.8	1945	7	US-10-094-749-1589	Sequence 1589, Ap
c 127	35	77.8	2542	8	US-10-437-963-51797	Sequence 51797, A
c 128	35	77.8	3011	8	US-10-437-963-40436	Sequence 40436, A
c 129	35	77.8	3196	8	US-10-437-963-75120	Sequence 75120, A
130	35	77.8	3918	10	US-10-499-353A-249	Sequence 249, App
131	35	77.8	4341	10	US-10-499-353A-248	Sequence 248, App
132	35	77.8	5455	10	US-10-499-353A-247	Sequence 247, App
133	35	77.8	7664	10	US-10-499-353A-246	Sequence 246, App
134	35	77.8	7676	8	US-10-042-865-11	Sequence 11, Appl
135	35	77.8	7728	10	US-10-499-353A-245	Sequence 245, App
136	35	77.8	7826	7	US-10-377-035-11	Sequence 11, Appl
137	35	77.8	7862	7	US-10-288-798-32	Sequence 32, Appl
138	35	77.8	7862	8	US-10-362-892-32	Sequence 32, Appl
139	35	77.8	14838	4	US-09-754-468-38	Sequence 38, Appl
140	34	75.6	21	15	US-11-124-708-8	Sequence 8, Appli
141	34	75.6	192	3	US-09-923-876-4221	Sequence 4221, Ap
142	34	75.6	192	3	US-09-923-876-4221	Sequence 4221, Ap
143	34	75.6	370	3	US-09-917-800A-455	Sequence 455, App
144	34	75.6	558	12	US-10-301-480-288840	Sequence 288840,
145	34	75.6	558	12	US-10-301-480-902249	Sequence 902249,
146	34	75.6	561	4	US-09-925-065A-200209	Sequence 200209,
147	34	75.6	561	5	US-09-925-065A-200209	Sequence 200209,
148	34	75.6	858	9	US-10-425-115-1221	Sequence 1221, Ap
c 149	34	75.6	1521	13	US-11-097-143-23465	Sequence 23465, A
150	34	75.6	1632	8	US-10-437-963-98481	Sequence 98481, A

ALIGNMENTS

RESULT 1
 US-10-411-910A-110
 ; Sequence 110, Application US/10411910A

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-185.rni.

[start](#)

[Go Back to previous pag](#)

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 20:00:56 ; Search time 146 Seconds
(without alignments)
307.580 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075102_19409/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=150 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss03h -USER=US10763712_CCGN_1_1_252@runat_29062006_075102_19409
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : Issued_Patents_NA:*
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 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	43	95.6	2399	3	US-10-077-699C-8	Sequence 8, Appli
2	43	95.6	2421	3	US-10-077-699C-9	Sequence 9, Appli
3	43	95.6	2636	3	US-10-077-699C-7	Sequence 7, Appli
4	43	95.6	3265	3	US-10-077-699C-3	Sequence 3, Appli
5	43	95.6	5001	3	US-10-077-699C-1	Sequence 1, Appli
6	43	95.6	5208	3	US-10-077-699C-2	Sequence 2, Appli
7	36	80.0	1581	3	US-09-902-540-9170	Sequence 9170, Ap
8	36	80.0	11612	3	US-09-902-540-981	Sequence 981, App
9	35	77.8	1945	4	US-10-094-749-1589	Sequence 1589, Ap
c 10	33	73.3	420	3	US-09-134-001C-2490	Sequence 2490, Ap
c 11	33	73.3	711	5	US-09-974-300-310	Sequence 310, App
c 12	33	73.3	738	3	US-09-902-540-6220	Sequence 6220, Ap
13	33	73.3	936	3	US-09-902-540-4133	Sequence 4133, Ap
14	33	73.3	1169	3	US-09-902-540-332	Sequence 332, App
15	33	73.3	3123	3	US-09-134-001C-2528	Sequence 2528, Ap
16	33	73.3	18469	3	US-09-902-540-1205	Sequence 1205, Ap
c 17	32	71.1	182	3	US-09-270-767-11190	Sequence 11190, A
18	32	71.1	441	3	US-08-914-375C-50	Sequence 50, Appl
19	32	71.1	601	3	US-09-949-016-26448	Sequence 26448, A
20	32	71.1	601	3	US-09-949-016-80787	Sequence 80787, A
21	32	71.1	601	3	US-09-949-016-94397	Sequence 94397, A
c 22	32	71.1	675	3	US-09-489-039A-2041	Sequence 2041, Ap
23	32	71.1	700	3	US-09-735-271-1290	Sequence 1290, Ap
24	32	71.1	700	3	US-09-533-559-5888	Sequence 5888, Ap
25	32	71.1	1002	3	US-08-426-630-7	Sequence 7, Appli
c 26	32	71.1	1644	3	US-09-489-039A-6672	Sequence 6672, Ap
c 27	32	71.1	1842	3	US-09-252-991A-4840	Sequence 4840, Ap
28	32	71.1	3573	3	US-09-252-991A-4903	Sequence 4903, Ap
29	32	71.1	5398	3	US-08-426-630-1	Sequence 1, Appli
c 30	32	71.1	5643	3	US-09-079-415-5	Sequence 5, Appli
c 31	32	71.1	5643	3	US-08-750-458A-1	Sequence 1, Appli
c 32	32	71.1	11620	3	US-09-902-540-1010	Sequence 1010, Ap
c 33	32	71.1	25010	3	US-09-949-016-14070	Sequence 14070, A
34	32	71.1	47476	3	US-09-949-016-12179	Sequence 12179, A
35	32	71.1	47476	3	US-09-949-016-14472	Sequence 14472, A
c 36	32	71.1	54550	3	US-10-327-189-42	Sequence 42, Appl
c 37	32	71.1	76164	3	US-09-949-016-12288	Sequence 12288, A
c 38	32	71.1	76165	3	US-09-949-016-14005	Sequence 14005, A
c 39	32	71.1	86936	3	US-09-949-016-17314	Sequence 17314, A
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c 144	31	68.9	252	3	US-08-441-971-43	Sequence 43, Appl
c 145	31	68.9	252	3	US-08-441-971-44	Sequence 44, Appl
c 146	31	68.9	252	3	US-08-441-971-45	Sequence 45, Appl
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ALIGNMENTS

RESULT 1

US-10-077-699C-8

; Sequence 8, Application US/10077699C

; Patent No. 6858718

; GENERAL INFORMATION:

; APPLICANT: Happe, Thomas

; TITLE OF INVENTION: Hydrogen Production

; FILE REFERENCE: 01MEL1

; CURRENT APPLICATION NUMBER: US/10/077,699C

; CURRENT FILING DATE: 2002-02-15

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rng.

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Ygapop 10.0 , Ygapext 0.5
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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SUMMARIES

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9	43	95.6	39	13	ADT91286	Adt91286 Fe-hydrog
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	44	42	93.3	1800	14	ADZ39224	Adz39224 Desulfovi
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c	50	36	80.0	3797	4	ABL23648	Abl23648 Drosophil
	51	36	80.0	11612	14	ACL64518	ACL64518 M. xanthu
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	88	33	73.3	714	13	ADT45463	Adt45463 Bacterial
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	92	33	73.3	936	14	ACL67670	ACL67670 M. xanthu
	93	33	73.3	1169	14	ACL63869	ACL63869 M. xanthu
	94	33	73.3	1290	12	ADP67804	Adp67804 Maize G34
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103	33	73.3	3556	5	ADL45389	Adl45389 Human ova
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105	33	73.3	10992	4	ABL05242	Abl05242 Drosophil
106	33	73.3	18469	14	ACL64742	AcL64742 M. xanthu
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c 134	32	71.1	5643	2	AAT09946	Aat09946 Aspergill
c 135	32	71.1	5643	2	AAT97394	Aat97394 Aspergill
136	32	71.1	7565	4	ABL29454	Abl29454 Drosophil
c 137	32	71.1	11358	10	ADC26983	Adc26983 Sorangium
c 138	32	71.1	11620	14	ACL64547	AcL64547 M. xanthu
c 139	32	71.1	18930	8	ACA43739	Aca43739 Prokaryot
c 140	32	71.1	37096	3	AAA81489_8	Continuation (9 of
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ALIGNMENTS

RESULT 1

ADT91297

ID ADT91297 standard; DNA; 39 BP.

XX

AC ADT91297;

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rapbn.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:32:53 ; Search time 16 Seconds
(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-10-449-902-46695

; Sequence 46695, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 46695

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-46695

Query Match 68.9%; Score 31; DB 6; Length 177;

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44.116 Million cell updates/sec

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Perfect score: 45
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Total number of hits satisfying chosen parameters: 2097797

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Listing first 150 summaries

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SUMMARIES

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ALIGNMENTS

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; Sequence 130, Application US/10763712A

; Publication No. US20050266541A1

; GENERAL INFORMATION:

; APPLICANT: Solazyme, Inc.

; APPLICANT: Dillon, Harrison F.

; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen

; TITLE OF INVENTION: Production

; FILE REFERENCE: H2042101-CIP

; CURRENT APPLICATION NUMBER: US/10/763,712A

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US 10/287,750

; PRIOR FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: US 10/411,910

; PRIOR FILING DATE: 2003-04-12

; PRIOR APPLICATION NUMBER: US 60/500,032

; PRIOR FILING DATE: 2003-09-03

; NUMBER OF SEQ ID NOS: 184

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 130

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic sequence

US-10-763-712A-130

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b 185.ra1.

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Title: US-10-763-712B-185
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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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SUMMARIES

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147	28	62.2	147	2	US-08-488-225A-97	Sequence 97, Appl
148	28	62.2	147	2	US-09-200-919-4	Sequence 4, Appli
149	28	62.2	147	2	US-10-679-999-6	Sequence 6, Appli
150	28	62.2	148	1	US-08-429-362-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-077-699C-6

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; Sequence 6, Application US/10077699C
; Patent No. 6858718
; GENERAL INFORMATION:
; APPLICANT: Happe, Thomas
; TITLE OF INVENTION: Hydrogen Production
; FILE REFERENCE: 01MEL1
; CURRENT APPLICATION NUMBER: US/10/077,699C
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Chlorella fusca
US-10-077-699C-6
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Query Match          95.6%;   Score 43;   DB 2;   Length 436;
Best Local Similarity 69.2%;   Pred. No. 0.86;
Matches      9;   Conservative    0;   Mismatches    4;   Indels      0;   Gaps      0;
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```
Qy      4 FXXXGGVMEAXR 16
          |  |||||  |
Db     261 FGTTGGVMEALR 273
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RESULT 2

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rag.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:18:54 ; Search time 185.333 Seconds
(without alignments)
39.472 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	13	8	ADT91236	Adt91236 Fe-hydrog
2	45	100.0	19	9	AEB73344	Aeb73344 Segment o
3	45	100.0	589	9	AEB73312	Aeb73312 Segment o
4	45	100.0	589	9	AEB73236	Aeb73236 Segment o
5	44	97.8	13	8	ADT91269	Adt91269 Fe-hydrog
6	44	97.8	13	8	ADT91253	Adt91253 Fe-hydrog
7	44	97.8	13	8	ADT91259	Adt91259 Fe-hydrog
8	44	97.8	13	8	ADT91266	Adt91266 Fe-hydrog
9	44	97.8	13	8	ADT91271	Adt91271 Fe-hydrog
10	44	97.8	19	9	AEB73591	Aeb73591 Fragment
11	43	95.6	13	8	ADT91227	Adt91227 Fe-hydrog
12	43	95.6	13	8	ADT91270	Adt91270 Fe-hydrog
13	43	95.6	13	8	ADT91273	Adt91273 Fe-hydrog
14	43	95.6	13	8	ADT91274	Adt91274 Fe-hydrog
15	43	95.6	13	8	ADT91267	Adt91267 Fe-hydrog
16	43	95.6	13	8	ADT91268	Adt91268 Fe-hydrog
17	43	95.6	13	8	ADT91272	Adt91272 Fe-hydrog
18	43	95.6	13	8	ADT91262	Adt91262 Fe-hydrog
19	43	95.6	13	8	ADT91231	Adt91231 Fe-hydrog
20	43	95.6	13	8	ADT91254	Adt91254 Fe-hydrog
21	43	95.6	13	8	ADT91225	Adt91225 Fe-hydrog
22	43	95.6	13	8	ADT91260	Adt91260 Fe-hydrog
23	43	95.6	17	10	AEE87520	Aee87520 Iron hydr
24	43	95.6	17	10	AEE87523	Aee87523 Iron hydr
25	43	95.6	17	10	AEE87519	Aee87519 Iron hydr
26	43	95.6	19	9	AEB73342	Aeb73342 Segment o
27	43	95.6	19	9	AEB73353	Aeb73353 Segment o
28	43	95.6	19	9	AEB73355	Aeb73355 Segment o
29	43	95.6	19	9	AEB73351	Aeb73351 Segment o
30	43	95.6	19	9	AEB73354	Aeb73354 Segment o
31	43	95.6	19	9	AEB73348	Aeb73348 Segment o
32	43	95.6	19	9	AEB73341	Aeb73341 Segment o
33	43	95.6	19	9	AEB73345	Aeb73345 Segment o
34	43	95.6	19	9	AEB73347	Aeb73347 Segment o
35	43	95.6	19	9	AEB73350	Aeb73350 Segment o
36	43	95.6	19	9	AEB73338	Aeb73338 Segment o
37	43	95.6	25	9	AEB73593	Aeb73593 Fragment
38	43	95.6	332	8	ADU00337	Adu00337 Iron hydr
39	43	95.6	332	8	ADU00338	Adu00338 Iron hydr
40	43	95.6	374	8	ADU00343	Adu00343 CpI catal
41	43	95.6	386	8	ADU00341	Adu00341 Iron hydr
42	43	95.6	388	8	ADU00342	Adu00342 Iron hydr
43	43	95.6	393	8	ADU00340	Adu00340 Iron hydr
44	43	95.6	403	9	AEB73241	Aeb73241 Segment o
45	43	95.6	410	9	AEB73299	Aeb73299 Segment o
46	43	95.6	415	9	AEB73239	Aeb73239 Segment o
47	43	95.6	436	9	ADY27750	Ady27750 Chlorella
48	43	95.6	436	9	AEB73219	Aeb73219 Segment o
49	43	95.6	448	9	ADY27748	Ady27748 Scenedesm
50	43	95.6	449	9	AEB73297	Aeb73297 Segment o
51	43	95.6	497	9	ADY27749	Ady27749 Chlamydom
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53	43	95.6	497	9	AEB73238	Aeb73238 Segment o
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55	43	95.6	505	9	AEB73303	Aeb73303 Segment o
56	43	95.6	505	9	AEB73337	Aeb73337 Gas chann
57	43	95.6	505	9	AEB73240	Aeb73240 Segment o

58	43	95.6	554	9	AEB73247	Aeb73247	Segment o
59	43	95.6	572	9	AEB73251	Aeb73251	Segment o
60	43	95.6	572	9	AEB73324	Aeb73324	Segment o
61	43	95.6	572	9	AEB73224	Aeb73224	Segment o
62	43	95.6	572	9	AEB73323	Aeb73323	Segment o
63	43	95.6	572	9	AEB73225	Aeb73225	Segment o
64	43	95.6	574	9	AEB73215	Aeb73215	Segment o
65	43	95.6	574	9	AEB73220	Aeb73220	Segment o
66	43	95.6	574	9	AEB73316	Aeb73316	Segment o
67	43	95.6	578	9	AEB73248	Aeb73248	Segment o
68	43	95.6	579	9	AEB73308	Aeb73308	Segment o
69	43	95.6	580	6	ABU24770	Abu24770	Protein e
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71	43	95.6	581	9	AEB73242	Aeb73242	Segment o
72	43	95.6	582	6	ABU24101	Abu24101	Protein e
73	43	95.6	582	7	ADC59546	Adc59546	Clostridi
74	43	95.6	582	8	ADR90318	Adr90318	Clostridi
75	43	95.6	582	9	AEB73237	Aeb73237	Segment o
76	43	95.6	582	9	AEB73315	Aeb73315	Segment o
77	43	95.6	588	9	AEB73309	Aeb73309	Segment o
78	43	95.6	606	9	AEB73223	Aeb73223	Segment o
79	43	95.6	606	9	AEB73300	Aeb73300	Segment o
80	43	95.6	606	9	AEB73311	Aeb73311	Segment o
81	43	95.6	619	9	AEB73249	Aeb73249	Segment o
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83	42	93.3	13	8	ADT91232	Adt91232	Fe-hydrog
84	42	93.3	13	8	ADT91256	Adt91256	Fe-hydrog
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89	42	93.3	13	8	ADT91246	Adt91246	Fe-hydrog
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93	42	93.3	13	8	ADT91245	Adt91245	Fe-hydrog
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95	42	93.3	13	8	ADT91250	Adt91250	Fe-hydrog
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97	42	93.3	13	8	ADT91264	Adt91264	Fe-hydrog
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105	42	93.3	13	8	ADT91243	Adt91243	Fe-hydrog
106	42	93.3	17	10	AEE87521	Aee87521	Iron hydr
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108	42	93.3	17	10	AEE87524	Aee87524	Iron hydr
109	42	93.3	19	9	AEB73349	Aeb73349	Segment o
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111	42	93.3	19	9	AEB73340	Aeb73340	Segment o
112	42	93.3	19	9	AEB73343	Aeb73343	Segment o
113	42	93.3	19	9	AEB73339	Aeb73339	Segment o
114	42	93.3	319	8	ADU00339	Adu00339	Iron hydr
115	42	93.3	379	9	AEB73254	Aeb73254	Segment o
116	42	93.3	389	9	AEB73245	Aeb73245	Segment o
117	42	93.3	421	9	AEB73229	Aeb73229	Segment o
118	42	93.3	421	9	AEB73227	Aeb73227	Segment o

119	42	93.3	421	9	AEB73216	Aeb73216 Segment o
120	42	93.3	421	9	AEB73255	Aeb73255 Segment o
121	42	93.3	421	9	AEB73317	Aeb73317 Segment o
122	42	93.3	421	9	AEB73221	Aeb73221 Segment o
123	42	93.3	439	9	AEB73253	Aeb73253 Segment o
124	42	93.3	449	9	AEB73318	Aeb73318 Segment o
125	42	93.3	449	9	AEB73235	Aeb73235 Segment o
126	42	93.3	458	9	AEB73246	Aeb73246 Segment o
127	42	93.3	468	9	AEB73234	Aeb73234 Segment o
128	42	93.3	468	9	AEB73314	Aeb73314 Segment o
129	42	93.3	484	9	AEB73226	Aeb73226 Segment o
130	42	93.3	555	9	AEB73244	Aeb73244 Segment o
131	42	93.3	608	9	AEB73230	Aeb73230 Segment o
132	42	93.3	608	9	AEB73304	Aeb73304 Segment o
133	42	93.3	636	9	AEB73243	Aeb73243 Segment o
134	42	93.3	636	9	AEB73307	Aeb73307 Segment o
135	42	93.3	1206	9	AEB73232	Aeb73232 Segment o
136	42	93.3	1206	9	AEB73313	Aeb73313 Segment o
137	41	91.1	13	8	ADT91247	Adt91247 Fe-hydrog
138	41	91.1	13	8	ADT91248	Adt91248 Fe-hydrog
139	41	91.1	13	8	ADT91224	Adt91224 Fe-hydrog
140	41	91.1	13	8	ADT91239	Adt91239 Fe-hydrog
141	41	91.1	13	8	ADT91241	Adt91241 Fe-hydrog
142	41	91.1	13	8	ADT91242	Adt91242 Fe-hydrog
143	41	91.1	13	8	ADT91249	Adt91249 Fe-hydrog
144	41	91.1	13	8	ADT91244	Adt91244 Fe-hydrog
145	41	91.1	16	9	AEB73399	Aeb73399 Segment o
146	40	88.9	13	8	ADT91238	Adt91238 Fe-hydrog
147	38	84.4	9	8	ADT91304	Adt91304 Fe-hydrog
148	38	84.4	10	9	ADY27757	Ady27757 Iron hydr
149	38	84.4	19	9	AEB73346	Aeb73346 Segment o
150	38	84.4	585	9	AEB73228	Aeb73228 Segment o

ALIGNMENTS

RESULT 1
 ADT91236
 ID ADT91236 standard; peptide; 13 AA.
 XX
 AC ADT91236;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Fe-hydrogenase motif #13.
 XX
 KW Iron hydrogenase; enzyme.
 XX
 OS Unidentified.
 XX
 PN US2004209256-A1.
 XX
 PD 21-OCT-2004.
 XX
 PF 12-APR-2003; 2003US-00411910.
 XX
 PR 12-APR-2003; 2003US-00411910.
 XX
 PA (SOLA-) SOLAZYME INC.
 XX

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rge.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:33:54 ; Search time 4514.67 Seconds
(without alignments)
339.945 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10763712_CCGN_1_1_5767@runat_29062006_075057_19242 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
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 5: gb_pr:*
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 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	45	100.0	1848	13	AF262401	AF262401 Trichomon
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3	43	95.6	546	1	AY660732	AY660732 Unculture
4	43	95.6	546	1	AY660738	AY660738 Unculture
5	43	95.6	549	1	AY660735	AY660735 Unculture
6	43	95.6	549	1	AY660736	AY660736 Unculture
7	43	95.6	654	1	DQ298810	DQ298810 Unculture
8	43	95.6	654	1	DQ298817	DQ298817 Unculture
9	43	95.6	654	1	DQ298821	DQ298821 Unculture
10	43	95.6	654	1	DQ298822	DQ298822 Unculture
11	43	95.6	654	1	DQ298828	DQ298828 Unculture
12	43	95.6	657	1	DQ225319	DQ225319 Unculture
13	43	95.6	657	1	DQ225320	DQ225320 Unculture
14	43	95.6	657	1	DQ298809	DQ298809 Unculture
15	43	95.6	657	1	DQ298820	DQ298820 Unculture
16	43	95.6	663	1	DQ225305	DQ225305 Unculture
17	43	95.6	663	1	DQ225306	DQ225306 Unculture
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39	43	95.6	696	15	AY652730	AY652730 Clostridi
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41	43	95.6	1518	4	AY436606	AY436606 Chlamydom
42	43	95.6	1607	4	AF276706	AF276706 Scenedesm
43	43	95.6	1831	15	AB016820	AB016820 Clostridi
44	43	95.6	1853	4	AY578072	AY578072 Chlamydom
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47	43	95.6	2267	15	CAU09760	U09760 Clostridium
48	43	95.6	2310	15	CLOHDCI	M81737 Clostridium
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53	43	95.6	2421	2	AR641148	AR641148 Sequence
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59	43	95.6	3230	15	AB016775	AB016775 Clostridi
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65	43	95.6	5001	4	SOB271546	AJ271546 Scenedesm
66	43	95.6	5208	2	AR641144	AR641144 Sequence
67	43	95.6	5999	4	CRE308413	AJ308413 Chlamydom
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70	43	95.6	16133	15	EAC312124	AJ312124 Eubacteri
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c 73	43	95.6	110000	15	CP000142_29	Continuation (30 o
c 74	43	95.6	110000	15	CP000232_17	Continuation (18 o
c 75	43	95.6	110000	15	CP000252_11	Continuation (12 o
c 76	43	95.6	110000	15	CR522870_04	Continuation (5 of
c 77	43	95.6	110000	15	CR522870_05	Continuation (6 of
78	43	95.6	110000	15	AE014299_40	Continuation (41 o
c 79	43	95.6	110000	15	AE015928_01	Continuation (2 of
c 80	43	95.6	110000	15	AE017226_16	Continuation (17 o
c 81	43	95.6	110000	15	AE017285_18	Continuation (19 o
82	43	95.6	110000	15	AJ965256_01	Continuation (2 of
83	43	95.6	110000	15	AP006840_34	Continuation (35 o
c 84	43	95.6	110000	15	BA000016_26	Continuation (27 o
c 85	43	95.6	110000	15	BA000016_27	Continuation (28 o
86	43	95.6	110000	15	CP000027_01	Continuation (2 of
c 87	43	95.6	349315	15	BX572593	BX572593 Rhodopseu
88	42	93.3	546	1	AY660733	AY660733 Unculture
89	42	93.3	546	1	AY660734	AY660734 Unculture
90	42	93.3	660	1	DQ225309	DQ225309 Unculture
91	42	93.3	660	1	DQ225315	DQ225315 Unculture
92	42	93.3	660	1	DQ225322	DQ225322 Unculture
93	42	93.3	660	1	DQ298807	DQ298807 Unculture
94	42	93.3	660	1	DQ298808	DQ298808 Unculture
95	42	93.3	660	1	DQ298818	DQ298818 Unculture
96	42	93.3	660	1	DQ298819	DQ298819 Unculture
97	42	93.3	660	1	DQ298829	DQ298829 Unculture
98	42	93.3	690	1	DQ225307	DQ225307 Unculture

99	42	93.3	690	1	DQ225321	DQ225321 Unculture
100	42	93.3	690	1	DQ298815	DQ298815 Unculture
101	42	93.3	690	1	DQ298827	DQ298827 Unculture
102	42	93.3	690	1	DQ298830	DQ298830 Unculture
103	42	93.3	1337	4	AF516683	AF516683 Neocallim
104	42	93.3	1544	2	CS073824	CS073824 Sequence
105	42	93.3	1544	13	TVU19897	U19897 Trichomonas
106	42	93.3	1659	13	TVU26964	U26964 Trichomonas
107	42	93.3	1761	4	AF446076	AF446076 Piromyces
108	42	93.3	1800	2	CS073820	CS073820 Sequence
109	42	93.3	1800	15	AF331719	AF331719 Desulfovi
110	42	93.3	1964	2	CS073819	CS073819 Sequence
111	42	93.3	1964	15	DVUHYDFE	M27212 D.vulgaris
112	42	93.3	2067	15	DVHYDG	X02416 Desulfovibr
113	42	93.3	2467	4	AY033895	AY033895 Neocallim
114	42	93.3	2585	15	AF120457	AF120457 Megasphe
115	42	93.3	2887	15	DFHYDABG	Y11759 D.fructosov
116	42	93.3	3625	13	NYHYDROG	Y16775 Nyctotherus
117	42	93.3	3933	13	AY608627	AY608627 Nyctother
118	42	93.3	110000	15	AE000512_02	Continuation (3 of
119	42	93.3	110000	15	CP000112_00	CP000112 Desulfovi
120	42	93.3	110000	15	CP000112_04	Continuation (5 of
c 121	42	93.3	110000	15	CP000112_22	Continuation (23 o
c 122	42	93.3	110000	15	CP000112_23	Continuation (24 o
c 123	42	93.3	110000	15	CP000142_18	Continuation (19 o
c 124	42	93.3	110000	15	CP000142_19	Continuation (20 o
125	42	93.3	110000	15	AE017285_18	Continuation (19 o
126	40	88.9	663	1	DQ298826	DQ298826 Unculture
127	39	86.7	546	1	AY660730	AY660730 Unculture
128	39	86.7	714	15	AY652731	AY652731 Clostridi
129	39	86.7	714	15	AY652732	AY652732 Clostridi
130	39	86.7	110000	15	BX571966_03	Continuation (4 of
c 131	39	86.7	110000	15	CP000011_19	Continuation (20 o
132	38	84.4	662	7	BV412230	BV412230 S229P6283
133	38	84.4	2439	2	CQ843465	CQ843465 Sequence
134	38	84.4	2439	5	AK126441	AK126441 Homo sapi
135	38	84.4	5251	15	DFU07229	U07229 Desulfovibr
136	38	84.4	68326	5	AC011283	AC011283 Homo sapi
137	38	84.4	110000	15	CP000142_18	Continuation (19 o
c 138	38	84.4	110000	15	AE017221_14	Continuation (15 o
139	38	84.4	167348	12	AC013782	AC013782 Homo sapi
140	38	84.4	173960	5	AC093885	AC093885 Homo sapi
c 141	37	82.2	11722	15	AE010432	AE010432 Methanopy
142	37	82.2	68100	4	AFA14E5	AL683874 Aspergill
c 143	37	82.2	89888	12	AY294423_3	Continuation (4 of
c 144	37	82.2	110000	15	AJ965256_04	Continuation (5 of
c 145	37	82.2	110000	15	CP000027_05	Continuation (6 of
146	37	82.2	141756	5	AL355382	AL355382 Human DNA
c 147	37	82.2	158483	12	AC015548	AC015548 Homo sapi
148	37	82.2	161371	6	AC132590	AC132590 Mus muscu
149	37	82.2	193170	12	AC068652	AC068652 Mus muscu
c 150	37	82.2	200472	6	AC162035	AC162035 Mus muscu

ALIGNMENTS

RESULT 1

AF262401

LOCUS AF262401 1848 bp mRNA linear INV 09-NOV-2000

DEFINITION Trichomonas vaginalis putative 64kDa iron hydrogenase mRNA, partial cds.

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-185.rst.

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This page gives you Search Results detail for the Application 10763712 and Search Result us-10-763-712b-185.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 29, 2006, 19:47:05 ; Search time 4942.67 Seconds
(without alignments)
271.526 Million cell updates/sec

Title: US-10-763-712B-185
Perfect score: 45
Sequence: 1 XXXFXXXGGVMEAAAXR 16

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075100_19328/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10763712@CGN_1_1_12067@runat_29062006_075100_19328 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	45	100.0	601	8	CV216049	CV216049 EST875759
c 2	45	100.0	603	8	CV216048	CV216048 EST875758
3	45	100.0	836	8	CV210634	CV210634 EST870344
4	45	100.0	883	8	CV209967	CV209967 EST869677
c 5	45	100.0	973	8	CV209966	CV209966 EST869676
c 6	45	100.0	1033	8	CV210633	CV210633 EST870343
7	43	95.6	549	7	BE337478	BE337478 894046C04
8	43	95.6	617	2	BI999849	BI999849 1031079E0
9	43	95.6	644	2	BM003317	BM003317 1031109G0
10	43	95.6	658	2	BI726441	BI726441 1031085C0
11	43	95.6	1050	13	CW918425	CW918425 EDCA527TR
c 12	43	95.6	1118	13	CW934222	CW934222 EDCCN13TR
13	38	84.4	532	7	BE518304	BE518304 WHE0808_F
14	38	84.4	563	9	DB270347	DB270347 DB270347
15	38	84.4	563	9	DB277683	DB277683 DB277683
16	38	84.4	564	9	DB277650	DB277650 DB277650
17	38	84.4	616	5	CD878589	CD878589 AZO4.103C
18	38	84.4	694	5	CD872019	CD872019 AZO2.119K
19	38	84.4	758	4	CB336646	CB336646 Tc021E12F
20	38	84.4	951	2	BG539706	BG539706 602567670
c 21	37	82.2	532	2	BG098351	BG098351 EST462870
22	37	82.2	592	4	CA006652	CA006652 HU05F03r
c 23	37	82.2	698	10	DV155376	DV155376 CV03097B2
24	36	80.0	221	13	CZ487899	CZ487899 f05264-5p
c 25	36	80.0	352	4	BY048856	BY048856 BY048856
26	36	80.0	361	11	AQ462547	AQ462547 HS_5213_A
c 27	36	80.0	429	1	AU078680	AU078680 AU078680
c 28	36	80.0	610	7	BF490206	BF490206 AT26517.5
c 29	36	80.0	636	4	CB647679	CB647679 OSJNEb10L
c 30	36	80.0	687	7	BF498871	BF498871 AT13281.5
c 31	36	80.0	698	7	BF500291	BF500291 AT15136.5
c 32	36	80.0	701	7	BF493192	BF493192 AT01494.5
c 33	36	80.0	704	7	BF493667	BF493667 AT01991.5
c 34	36	80.0	705	7	BF493579	BF493579 AT01880.5
c 35	36	80.0	714	4	CB647837	CB647837 OSJNEb10P
c 36	36	80.0	730	7	BF506037	BF506037 AT08391.5
c 37	36	80.0	1022	3	BQ714256	BQ714256 AGENCOURT
c 38	35	77.8	298	2	BI059695	BI059695 MR4-UT005

c	39	35	77.8	318	5	CI285736	CI285736 CI285736
	40	35	77.8	344	4	C28416	C28416 C28416 Rice
c	41	35	77.8	362	10	DV168716	DV168716 ZM_BFb016
	42	35	77.8	367	11	AZ920964	AZ920964 1006023A0
	43	35	77.8	372	5	CI291090	CI291090 CI291090
	44	35	77.8	377	9	DN999534	DN999534 TC104360
	45	35	77.8	383	8	CV723806	CV723806 root--04-
	46	35	77.8	392	5	CF990916	CF990916 18317rsic
c	47	35	77.8	405	4	BY308010	BY308010 BY308010
c	48	35	77.8	425	9	DN141900	DN141900 5036_D03_
c	49	35	77.8	429	5	CI296013	CI296013 CI296013
	50	35	77.8	442	7	BF040679	BF040679 BP250002A
c	51	35	77.8	454	12	CC032111	CC032111 3591_1_12
	52	35	77.8	459	5	CF984650	CF984650 15258rsic
	53	35	77.8	470	5	CI309180	CI309180 CI309180
	54	35	77.8	472	9	DN106393	DN106393 1103768 M
	55	35	77.8	475	4	BY158321	BY158321 BY158321
c	56	35	77.8	489	12	CC020874	CC020874 3591_1_21
c	57	35	77.8	499	8	CO532607	CO532607 3530_1_21
	58	35	77.8	500	5	CF984527	CF984527 17633rsic
	59	35	77.8	514	14	CT105399	CT105399 Sus scrof
	60	35	77.8	532	5	CF990543	CF990543 17881rsic
	61	35	77.8	534	7	BF044803	BF044803 BP250019A
	62	35	77.8	537	10	DW992503	DW992503 EST44884
c	63	35	77.8	549	10	DV535776	DV535776 ZM_BFb022
	64	35	77.8	554	9	DA622709	DA622709 DA622709
c	65	35	77.8	573	10	DR808400	DR808400 ZM_BFb003
c	66	35	77.8	579	2	BF913740	BF913740 MR4-UT005
c	67	35	77.8	580	8	CV663568	CV663568 LCPE04EX0
c	68	35	77.8	586	10	DV513661	DV513661 ZM_BFb019
c	69	35	77.8	587	10	DY232992	DY232992 ZM_BFb024
c	70	35	77.8	588	13	CZ555896	CZ555896 M0029301
	71	35	77.8	598	7	BF380280	BF380280 MR4-UT005
c	72	35	77.8	604	14	CNS04032	AL268391 Tetraodon
	73	35	77.8	605	10	DW552619	DW552619 EST_ss1_
c	74	35	77.8	611	10	DV541347	DV541347 ZM_BFb023
	75	35	77.8	621	2	BG573944	BG573944 602593393
c	76	35	77.8	639	12	CG351362	CG351362 OGXAN07TH
	77	35	77.8	642	14	DX272345	DX272345 OR_ABa016
	78	35	77.8	646	4	CA758423	CA758423 BR0500150
	79	35	77.8	650	5	CI136609	CI136609 CI136609
	80	35	77.8	650	5	CI138269	CI138269 CI138269
c	81	35	77.8	655	5	CD216274	CD216274 pgp2n.pk0
c	82	35	77.8	656	12	CG288985	CG288985 OG1BD33TV
c	83	35	77.8	666	10	DV536364	DV536364 ZM_BFb022
c	84	35	77.8	672	4	CA194351	CA194351 SCRFSB102
	85	35	77.8	674	13	CL611557	CL611557 OR_BB000
c	86	35	77.8	675	10	DT641459	DT641459 ZM_BFb009
c	87	35	77.8	681	10	DV030843	DV030843 ZM_BFb015
	88	35	77.8	700	5	CI138741	CI138741 CI138741
	89	35	77.8	700	5	CI255938	CI255938 CI255938
	90	35	77.8	700	5	CI256212	CI256212 CI256212
c	91	35	77.8	700	14	AG108792	AG108792 Pan trogl
c	92	35	77.8	721	10	DV532539	DV532539 ZM_BFb022
c	93	35	77.8	725	4	CB644939	CB644939 OSJNEb06F
c	94	35	77.8	728	4	CB651572	CB651572 OSJNEb16J
c	95	35	77.8	731	4	CB642456	CB642456 OSJNEb02K
c	96	35	77.8	740	3	BU106381	BU106381 603007091
	97	35	77.8	741	4	CB653991	CB653991 OSJNEc05I
c	98	35	77.8	745	4	CB642552	CB642552 OSJNEb02M
c	99	35	77.8	747	4	CB653992	CB653992 OSJNEc05I

c 100	35	77.8	749	4	CB648890	CB648890 OSJNEb12I
c 101	35	77.8	750	10	DV502245	DV502245 ZM_BFb017
c 102	35	77.8	761	5	CK762050	CK762050 atr02-7ms
c 103	35	77.8	766	10	DR965772	DR965772 ZM_BFb008
104	35	77.8	774	4	CB648889	CB648889 OSJNEb12I
c 105	35	77.8	776	4	CB662606	CB662606 OSJNEd06M
c 106	35	77.8	778	10	DV020937	DV020937 ZM_BFb013
107	35	77.8	778	13	CL705690	CL705690 SP_Bb004
c 108	35	77.8	787	10	DR955386	DR955386 ZM_BFb004
c 109	35	77.8	792	10	DR814011	DR814011 ZM_BFb004
110	35	77.8	793	4	CB650095	CB650095 OSJNEb14F
c 111	35	77.8	794	4	CB650096	CB650096 OSJNEb14F
c 112	35	77.8	803	10	DR814506	DR814506 ZM_BFb004
113	35	77.8	806	4	CB642455	CB642455 OSJNEb02K
114	35	77.8	815	4	CB651571	CB651571 OSJNEb16J
115	35	77.8	819	4	CB651570	CB651570 OSJNEb16J
c 116	35	77.8	819	10	DR970188	DR970188 ZM_BFb009
117	35	77.8	825	4	CB645740	CB645740 OSJNEb07K
c 118	35	77.8	826	10	DR811791	DR811791 ZM_BFb004
c 119	35	77.8	827	10	DT942309	DT942309 ZM_BFb012
c 120	35	77.8	837	4	CB645741	CB645741 OSJNEb07K
121	35	77.8	845	4	CB677558	CB677558 OSJNEe14K
122	35	77.8	846	4	CB642551	CB642551 OSJNEb02M
123	35	77.8	875	12	BZ652401	BZ652401 OGCCW45TC
c 124	35	77.8	879	10	DR819123	DR819123 ZM_BFb005
125	35	77.8	890	4	CB644938	CB644938 OSJNEb06F
c 126	35	77.8	906	13	CL461908	CL461908 SAIL_1154
c 127	35	77.8	909	10	DR964150	DR964150 ZM_BFb008
128	35	77.8	914	8	CV089450	CV089450 est_c_vir
129	35	77.8	944	12	CG288361	CG288361 OGXCM32TH
c 130	35	77.8	1010	14	CNS03T9C	AL259545 Tetraodon
c 131	35	77.8	1029	13	CW923845	CW923845 EDCB082TR
132	35	77.8	1098	14	CNS03BCR	AL236340 Tetraodon
c 133	35	77.8	1109	2	BG110233	BG110233 602279886
134	35	77.8	1200	8	CX099889	CX099889 RECM0658
135	35	77.8	1952	6	BC018692	BC018692 Homo sapi
c 136	34	75.6	122	12	BZ596952	BZ596952 SALK_0979
137	34	75.6	195	5	CF558658	CF558658 1115039G1
138	34	75.6	234	7	AW433603	AW433603 UI-R-BJ0p
139	34	75.6	274	2	BG183978	BG183978 RST2893 A
140	34	75.6	300	1	AU115507	AU115507 AU115507
141	34	75.6	301	5	CK783132	CK783132 UI-D-GC1-
c 142	34	75.6	306	14	DX255468	DX255468 OR_ABa014
143	34	75.6	310	7	AW532409	AW532409 UI-R-BS0-
144	34	75.6	311	1	AI714009	AI714009 UI-R-AF1-
145	34	75.6	331	8	CR463215	CR463215 CR463215
146	34	75.6	338	1	AI010046	AI010046 EST204497
c 147	34	75.6	360	4	C68144	C68144 C68144 Yuji
148	34	75.6	370	1	AA997765	AA997765 UI-R-C0-h
149	34	75.6	373	7	BE105797	BE105797 UI-R-BX0-
150	34	75.6	381	7	AW253518	AW253518 UI-R-BJ0-

ALIGNMENTS

RESULT 1
CV216049
LOCUS CV216049 601 bp mRNA linear EST 16-SEP-2004
DEFINITION EST875759 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
clone TVTCC29 5' end, mRNA sequence.
ACCESSION CV216049

**SCORE Search Results Details for Application
10763712 and Search Result us-10-763-712b-
186.rst.**

Comments /
Suggestions

start

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      June 29, 2006, 19:47:05 ; Search time 2471.33 Seconds
              (without alignments)
              271.526 Million cell updates/sec
```

```
Title:      US-10-763-712B-186
Perfect score: 29
Sequence:   1 ADXTIXEE 8
```

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Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0
```

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries
```

```

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075100_19328/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10763712_CGN_1_1_12067_@runat_29062006_075100_19328 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database :      EST:*
           1:   qb est1:*
```

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	29	100.0	439	1	AA802002	AA802002 GM03708.5
2	29	100.0	512	10	DR446627	DR446627 AR1034D02
3	29	100.0	600	11	AZ440534	AZ440534 1M0231F12
4	29	100.0	620	1	AI114013	AI114013 GH10644.5
c 5	29	100.0	799	13	CL664979	CL664979 PRI0148c_
6	28	96.6	308	1	AV119417	AV119417 AV119417
c 7	28	96.6	358	11	AQ763009	AQ763009 HS_3191_B
8	28	96.6	392	4	CB376953	CB376953 Hb02A08 L
c 9	28	96.6	399	1	AI985747	AI985747 wr76h02.x
10	28	96.6	400	4	CB546520	CB546520 AMGNNUC:N
c 11	28	96.6	404	11	AZ929796	AZ929796 479.dil55
12	28	96.6	424	10	DY181351	DY181351 000217BOV
13	28	96.6	451	10	DW207354	DW207354 EST23618
14	28	96.6	494	2	BM522129	BM522129 ESSU0666
c 15	28	96.6	508	13	CZ769915	CZ769915 OC__Ba012
c 16	28	96.6	520	11	AQ853247	AQ853247 LMAJFV1_1
17	28	96.6	545	10	DW210560	DW210560 EST26824
18	28	96.6	548	12	CE712029	CE712029 tigr-gss-
19	28	96.6	549	1	AU199321	AU199321 AU199321
c 20	28	96.6	553	10	DR507779	DR507779 WS02720.B
21	28	96.6	558	10	DW205650	DW205650 EST21914
22	28	96.6	577	10	DW206113	DW206113 EST22377
c 23	28	96.6	579	10	DW992636	DW992636 EST45017
24	28	96.6	584	8	CV244922	CV244922 WS0255.B2
c 25	28	96.6	586	14	AG211417	AG211417 Oryza sat
26	28	96.6	595	10	DW201862	DW201862 EST18132
27	28	96.6	600	5	CD352191	CD352191 UI-M-GIO-
28	28	96.6	601	5	CK391979	CK391979 K0839C03-
29	28	96.6	611	1	AU206495	AU206495 AU206495
30	28	96.6	618	9	DR028491	DR028491 bda010051
c 31	28	96.6	621	11	AQ999205	AQ999205 RPCI-23-3
c 32	28	96.6	629	11	AQ047901	AQ047901 cLM-4a8-u
33	28	96.6	630	7	AW753457	AW753457 QV2-CT026
34	28	96.6	631	1	AU205723	AU205723 AU205723
35	28	96.6	631	8	CV223829	CV223829 CS_hyp_08
36	28	96.6	632	14	CT287874	CT287874 Sus scrof
37	28	96.6	634	5	CK617072	CK617072 mk01a05.y
c 38	28	96.6	639	8	CX173957	CX173957 B11_69-10

	39	28	96.6	641	13	CW482884	CW482884 fsbb001f2
c	40	28	96.6	654	13	CW482883	CW482883 fsbb001f2
	41	28	96.6	664	12	CE068236	CE068236 tigr-gss-
	42	28	96.6	668	12	CC946162	CC946162 BOIFG75TF
	43	28	96.6	671	10	DW212585	DW212585 EST28849
c	44	28	96.6	675	5	CF306407	CF306407 HDA1--03-
	45	28	96.6	677	10	DR525776	DR525776 WS02720.B
	46	28	96.6	678	10	DW219177	DW219177 EST35435
c	47	28	96.6	689	14	CR060167	CR060167 Forward s
	48	28	96.6	692	12	CE507471	CE507471 tigr-gss-
	49	28	96.6	694	8	CN359881	CN359881 170005315
c	50	28	96.6	700	8	CR373248	CR373248 CR373248
c	51	28	96.6	702	11	BH925823	BH925823 odi59c04.
c	52	28	96.6	703	11	BH651871	BH651871 BOHYA03TR
	53	28	96.6	708	13	CW519540	CW519540 OP__Ba002
	54	28	96.6	712	2	BI107985	BI107985 602902361
c	55	28	96.6	714	11	BH923230	BH923230 odi01h09.
	56	28	96.6	728	14	AG424374	AG424374 Mus muscu
	57	28	96.6	744	14	AG441044	AG441044 Mus muscu
	58	28	96.6	746	11	AZ133410	AZ133410 OSJNBb010
	59	28	96.6	754	8	CO247598	CO247598 AGENCOURT
	60	28	96.6	757	8	CR284966	CR284966 CR284966
c	61	28	96.6	758	11	BH582202	BH582202 BOGMU74TF
	62	28	96.6	759	14	AG424375	AG424375 Mus muscu
	63	28	96.6	770	10	DR523819	DR523819 WS02715.B
	64	28	96.6	782	2	BI665663	BI665663 603289659
c	65	28	96.6	784	5	CF817640	CF817640 EST695022
	66	28	96.6	786	5	CD656171	CD656171 AGENCOURT
c	67	28	96.6	789	11	BZ494093	BZ494093 BONHI51TR
	68	28	96.6	800	13	DU274767	DU274767 109844800
c	69	28	96.6	812	11	BH424746	BH424746 BOGUP64TR
	70	28	96.6	817	11	BH513858	BH513858 BOGYC15TR
	71	28	96.6	818	8	CV123638	CV123638 OSTF30015
	72	28	96.6	823	9	DR029231	DR029231 bda010072
	73	28	96.6	828	10	DT489984	DT489984 WS02543.B
	74	28	96.6	830	9	DR029576	DR029576 bda010082
	75	28	96.6	835	10	DR537717	DR537717 WS02752.C
	76	28	96.6	861	10	DT491462	DT491462 WS02547.C
c	77	28	96.6	866	13	DU119811	DU119811 KBrH101B1
c	78	28	96.6	878	14	CR241993	CR241993 Forward s
	79	28	96.6	885	10	DT525309	DT525309 WS02045.C
	80	28	96.6	889	13	DU083509	DU083509 279791 To
	81	28	96.6	914	10	DT489748	DT489748 WS02543.B
	82	28	96.6	917	3	BU178367	BU178367 AGENCOURT
	83	28	96.6	917	10	DT488741	DT488741 WS02537.B
	84	28	96.6	1005	3	BM564901	BM564901 AGENCOURT
	85	28	96.6	1082	3	BQ955528	BQ955528 AGENCOURT
c	86	28	96.6	1473	13	CL647975	CL647975 CH213-157
	87	28	96.6	5391	14	DQ037846	DQ037846 Homo sapi
	88	28	96.6	5391	14	DQ037847	DQ037847 Pan trogl
	89	27	93.1	145	12	BZ613479	BZ613479 KBrH13901
c	90	27	93.1	147	1	AI758327	AI758327 ty06d05.x
	91	27	93.1	157	4	BX610202	BX610202 BX610202
	92	27	93.1	178	4	CA364740	CA364740 639708 NC
	93	27	93.1	195	4	CB042710	CB042710 4007513 B
c	94	27	93.1	235	1	AV341479	AV341479 AV341479
	95	27	93.1	236	11	AQ586437	AQ586437 RPCI-11-4
c	96	27	93.1	269	8	CV626741	CV626741 zcm25g03.
	97	27	93.1	281	1	AA682378	AA682378 zj86b03.s
c	98	27	93.1	284	1	AV424451	AV424451 AV424451
	99	27	93.1	288	5	CD966095	CD966095 SEL_73 Ge

99	27	93.1	296	10	AF291129	AF291129	HIV-1	iso
100	27	93.1	296	10	AY877083	AY877083	HIV-1	iso
101	27	93.1	297	10	AF024856	AF024856	HIV-1	pat
102	27	93.1	297	10	AF024861	AF024861	HIV-1	pat
103	27	93.1	297	10	AF142228	AF142228	HIV-1	fro
104	27	93.1	297	10	AF142229	AF142229	HIV-1	fro
105	27	93.1	297	10	AF142231	AF142231	HIV-1	fro
106	27	93.1	297	10	AF142232	AF142232	HIV-1	fro
107	27	93.1	297	10	AF142233	AF142233	HIV-1	fro
108	27	93.1	297	10	AF142234	AF142234	HIV-1	fro
109	27	93.1	297	10	AF142235	AF142235	HIV-1	fro
110	27	93.1	297	10	AF142236	AF142236	HIV-1	fro
111	27	93.1	297	10	AF142238	AF142238	HIV-1	fro
112	27	93.1	297	10	AF142239	AF142239	HIV-1	fro
113	27	93.1	297	10	AF204326	AF204326	HIV-1	pat
114	27	93.1	297	10	AF204368	AF204368	HIV-1	pat
115	27	93.1	297	10	AF227687	AF227687	HIV-1	pat
116	27	93.1	297	10	AF227688	AF227688	HIV-1	pat
117	27	93.1	297	10	AF288796	AF288796	HIV-1	iso
118	27	93.1	297	10	AF288797	AF288797	HIV-1	iso
119	27	93.1	297	10	AF288804	AF288804	HIV-1	iso
120	27	93.1	297	10	AF311132	AF311132	HIV-1	iso
121	27	93.1	297	10	AF317024	AF317024	HIV-1	GR.
122	27	93.1	297	10	AF544416	AF544416	HIV-1	iso
123	27	93.1	297	10	AF544475	AF544475	HIV-1	iso
124	27	93.1	297	10	AF544509	AF544509	HIV-1	iso
125	27	93.1	297	10	AF544519	AF544519	HIV-1	iso
126	27	93.1	297	10	AF544554	AF544554	HIV-1	iso
127	27	93.1	297	10	AF544556	AF544556	HIV-1	iso
128	27	93.1	297	10	AF544560	AF544560	HIV-1	iso
129	27	93.1	297	10	AF544566	AF544566	HIV-1	iso
130	27	93.1	297	10	AF544571	AF544571	HIV-1	iso
131	27	93.1	297	10	AF544590	AF544590	HIV-1	iso
132	27	93.1	297	10	AF544611	AF544611	HIV-1	iso
133	27	93.1	297	10	AY182828	AY182828	HIV-1	iso
134	27	93.1	297	10	AY203678	AY203678	HIV-1	iso
135	27	93.1	297	10	AY203680	AY203680	HIV-1	iso
136	27	93.1	297	10	AY203681	AY203681	HIV-1	iso
137	27	93.1	297	10	AY203682	AY203682	HIV-1	iso
138	27	93.1	297	10	AY203683	AY203683	HIV-1	iso
139	27	93.1	297	10	AY203685	AY203685	HIV-1	iso
140	27	93.1	297	10	AY203687	AY203687	HIV-1	iso
141	27	93.1	297	10	AY203688	AY203688	HIV-1	iso
142	27	93.1	297	10	AY203689	AY203689	HIV-1	iso
143	27	93.1	297	10	AY305996	AY305996	HIV-1	iso
144	27	93.1	297	10	AY305999	AY305999	HIV-1	iso
145	27	93.1	297	10	AY313344	AY313344	HIV-1	iso
146	27	93.1	297	10	AY370055	AY370055	HIV-1	iso
147	27	93.1	297	10	AY370057	AY370057	HIV-1	iso
148	27	93.1	297	10	AY455412	AY455412	HIV-1	iso
149	27	93.1	297	10	AY502098	AY502098	HIV-1	iso
150	27	93.1	297	10	AY569833	AY569833	HIV-1	iso

ALIGNMENTS

RESULT 1

FCU06650

LOCUS FCU06650 658 bp RNA linear VRL 24-MAY-1995

DEFINITION Feline calicivirus FS capsid protein gene, partial cds.

ACCESSION U06650

SCORE Search Results Details for Application 10763712 and Search Result us-10-763-712b-186.rge.

Comments /
Suggestions

start

[Go Back to previous page](#)

GenCore version 5.1.9
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OM protein - nucleic search, using frame plus p2n model

```
Run on:      June 29, 2006, 19:33:54 ; Search time 2257.33 Seconds
              (without alignments)
              339.945 Million cell updates/sec
```

```
Title:      US-10-763-712B-186
Perfect score: 29
Sequence:   1 ADXTIXEE 8
```

```

Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0

```

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries
```

```
Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10763712/runat_29062006_075057_19242/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10763712_@CGN_1_1_5767_@runat_29062006_075057_19242 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      GenEmbl:*
           1:  gb env:*
```

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	658	10	FCU06650	U06650 Feline cali
	2	29	100.0	1098	13	DROPENFSB	M15765 D.melanogas
	3	29	100.0	1619	2	CQ579063	CQ579063 Sequence
	4	29	100.0	1620	13	DMU13178	U13178 Drosophila
	5	29	100.0	1652	13	BT004875	BT004875 Drosophil
	6	29	100.0	1657	13	DRORNABP	L37083 Drosophila
c	7	29	100.0	6664	2	CQ579062	CQ579062 Sequence
c	8	29	100.0	81181	12	AC019668	AC019668 Drosophil
c	9	29	100.0	110000	12	AP006485_0	AP006485 Cyanidios
c	10	29	100.0	155728	6	AC139325	AC139325 Mus muscu
c	11	29	100.0	169623	6	AC131581	AC131581 Mus muscu
	12	29	100.0	176969	13	AC010707	AC010707 Drosophil
	13	29	100.0	192540	13	AC010846	AC010846 Drosophil
	14	29	100.0	195753	12	AC128091	AC128091 Rattus no
	15	29	100.0	206259	12	AC156218	AC156218 Bos tauru
c	16	29	100.0	227299	6	AC138722	AC138722 Mus muscu
c	17	29	100.0	242568	12	AC134100	AC134100 Rattus no
	18	29	100.0	295650	15	BX294151	BX294151 Pirellula
	19	29	100.0	323840	13	AE003501	AE003501 Drosophil
	20	28	96.6	144	10	S61103	S61103 gag [avian
c	21	28	96.6	280	14	AB104398	AB104398 Equus cab
c	22	28	96.6	810	7	BV655660	BV655660 S217P6913
	23	28	96.6	3212	5	BC038232	BC038232 Homo sapi
	24	28	96.6	3566	4	AK065392	AK065392 Oryza sat
c	25	28	96.6	3807	4	AK069356	AK069356 Oryza sat
	26	28	96.6	4433	6	AK129390	AK129390 Mus muscu
	27	28	96.6	4706	2	CQ715465	CQ715465 Sequence
	28	28	96.6	5264	2	DD210151	DD210151 Methods o
	29	28	96.6	5323	2	AR578550	AR578550 Sequence
	30	28	96.6	6395	5	AB046769	AB046769 Homo sapi
	31	28	96.6	7548	6	BC079889	BC079889 Mus muscu
c	32	28	96.6	7693	15	AY509036	AY509036 Bifidobac
	33	28	96.6	10811	15	AE009306	AE009306 Agrobacte
c	34	28	96.6	10924	15	AE008308	AE008308 Agrobacte
	35	28	96.6	12393	15	AE012414	AE012414 Xanthomon
c	36	28	96.6	14000	2	CQ800374	CQ800374 Sequence
	37	28	96.6	37225	13	CEC17E4	Z81037 Caenorhabdi

c	38	28	96.6	37302	5	D87007	D87007 Homo sapien
c	39	28	96.6	43594	5	AC093144	AC093144 Homo sapi
	40	28	96.6	43840	13	CBRG45G04	AC084633 Caenorhab
c	41	28	96.6	106247	12	AC121232	AC121232 Medicago
	42	28	96.6	110000	4	AP008212_284	Continuation (285
c	43	28	96.6	110000	4	CR382123_12	Continuation (13 o
c	44	28	96.6	110000	4	CR382133_01	Continuation (2 of
	45	28	96.6	110000	12	AC129397_0	AC129397 Rattus no
	46	28	96.6	110000	12	CT005269_11	Continuation (12 o
	47	28	96.6	110000	15	CP000076_18	Continuation (19 o
c	48	28	96.6	110000	15	AY596297_05	Continuation (6 of
c	49	28	96.6	115996	4	AC146566	AC146566 Medicago
c	50	28	96.6	128946	12	AP007875	AP007875 Lotus cor
c	51	28	96.6	132114	5	AC026772	AC026772 Homo sapi
	52	28	96.6	137590	12	AC027567	AC027567 Homo sapi
	53	28	96.6	140682	5	HS283K11	AL024497 Human DNA
	54	28	96.6	143376	5	AC012331	AC012331 Homo sapi
c	55	28	96.6	144430	5	AC091155	AC091155 Homo sapi
c	56	28	96.6	146903	12	AC024410	AC024410 Homo sapi
c	57	28	96.6	151111	5	AC002308	AC002308 Homo sapi
	58	28	96.6	156495	12	AL157374	AL157374 Homo sapi
	59	28	96.6	163648	12	AC142370	AC142370 Rattus no
	60	28	96.6	166128	4	AP005457	AP005457 Oryza sat
	61	28	96.6	168509	5	AC009837	AC009837 Homo sapi
	62	28	96.6	169514	12	CT027648	CT027648 Danio rer
	63	28	96.6	170250	6	AC144648	AC144648 Mus muscu
c	64	28	96.6	173485	11	CR388028	CR388028 Zebrafish
c	65	28	96.6	174851	12	AC173325	AC173325 Bos tauru
c	66	28	96.6	176015	6	AC164003	AC164003 Mus muscu
	67	28	96.6	177220	6	AC102550	AC102550 Mus muscu
c	68	28	96.6	178146	12	AC121453	AC121453 Rattus no
	69	28	96.6	179273	12	AC134386	AC134386 Papio anu
c	70	28	96.6	186505	12	CT583651	CT583651 Danio rer
	71	28	96.6	188342	6	AC173966	AC173966 Mus muscu
c	72	28	96.6	200300	12	AC111531	AC111531 Rattus no
	73	28	96.6	206878	6	AC157667	AC157667 Mus muscu
c	74	28	96.6	211684	6	AC147637	AC147637 Mus muscu
	75	28	96.6	218522	6	AC154806	AC154806 Mus muscu
	76	28	96.6	224461	12	AC115419	AC115419 Rattus no
c	77	28	96.6	225586	11	BX469934	BX469934 Zebrafish
c	78	28	96.6	228760	12	AC129816	AC129816 Rattus no
c	79	28	96.6	228976	11	AC144489	AC144489 Gasterost
c	80	28	96.6	230334	6	AC112521	AC112521 Mus muscu
c	81	28	96.6	233946	6	AC156790	AC156790 Mus muscu
c	82	28	96.6	236791	6	AC167013	AC167013 Mus muscu
c	83	28	96.6	237455	12	AC096815	AC096815 Rattus no
	84	28	96.6	249667	12	AC114720	AC114720 Rattus no
c	85	28	96.6	269263	12	AC097883	AC097883 Rattus no
	86	28	96.6	294850	15	BX294148	BX294148 Pirellula
	87	28	96.6	308916	2	CQ870470	CQ870470 Sequence
	88	27	93.1	252	10	AY797550	AY797550 HIV-1 iso
	89	27	93.1	255	10	AY797637	AY797637 HIV-1 iso
	90	27	93.1	258	10	AY797965	AY797965 HIV-1 iso
	91	27	93.1	283	10	AY334917	AY334917 HIV-1 iso
	92	27	93.1	283	10	AY334966	AY334966 HIV-1 iso
	93	27	93.1	283	10	AY334981	AY334981 HIV-1 iso
	94	27	93.1	283	10	AY335008	AY335008 HIV-1 iso
	95	27	93.1	283	10	AY335011	AY335011 HIV-1 iso
	96	27	93.1	283	10	AY335039	AY335039 HIV-1 iso
	97	27	93.1	288	10	AY370056	AY370056 HIV-1 iso
	98	27	93.1	294	10	AY797136	AY797136 HIV-1 iso

99	27	93.1	296	10	AF291129	AF291129	HIV-1	iso
100	27	93.1	296	10	AY877083	AY877083	HIV-1	iso
101	27	93.1	297	10	AF024856	AF024856	HIV-1	pat
102	27	93.1	297	10	AF024861	AF024861	HIV-1	pat
103	27	93.1	297	10	AF142228	AF142228	HIV-1	fro
104	27	93.1	297	10	AF142229	AF142229	HIV-1	fro
105	27	93.1	297	10	AF142231	AF142231	HIV-1	fro
106	27	93.1	297	10	AF142232	AF142232	HIV-1	fro
107	27	93.1	297	10	AF142233	AF142233	HIV-1	fro
108	27	93.1	297	10	AF142234	AF142234	HIV-1	fro
109	27	93.1	297	10	AF142235	AF142235	HIV-1	fro
110	27	93.1	297	10	AF142236	AF142236	HIV-1	fro
111	27	93.1	297	10	AF142238	AF142238	HIV-1	fro
112	27	93.1	297	10	AF142239	AF142239	HIV-1	fro
113	27	93.1	297	10	AF204326	AF204326	HIV-1	pat
114	27	93.1	297	10	AF204368	AF204368	HIV-1	pat
115	27	93.1	297	10	AF227687	AF227687	HIV-1	pat
116	27	93.1	297	10	AF227688	AF227688	HIV-1	pat
117	27	93.1	297	10	AF288796	AF288796	HIV-1	iso
118	27	93.1	297	10	AF288797	AF288797	HIV-1	iso
119	27	93.1	297	10	AF288804	AF288804	HIV-1	iso
120	27	93.1	297	10	AF311132	AF311132	HIV-1	iso
121	27	93.1	297	10	AF317024	AF317024	HIV-1	GR.
122	27	93.1	297	10	AF544416	AF544416	HIV-1	iso
123	27	93.1	297	10	AF544475	AF544475	HIV-1	iso
124	27	93.1	297	10	AF544509	AF544509	HIV-1	iso
125	27	93.1	297	10	AF544519	AF544519	HIV-1	iso
126	27	93.1	297	10	AF544554	AF544554	HIV-1	iso
127	27	93.1	297	10	AF544556	AF544556	HIV-1	iso
128	27	93.1	297	10	AF544560	AF544560	HIV-1	iso
129	27	93.1	297	10	AF544566	AF544566	HIV-1	iso
130	27	93.1	297	10	AF544571	AF544571	HIV-1	iso
131	27	93.1	297	10	AF544590	AF544590	HIV-1	iso
132	27	93.1	297	10	AF544611	AF544611	HIV-1	iso
133	27	93.1	297	10	AY182828	AY182828	HIV-1	iso
134	27	93.1	297	10	AY203678	AY203678	HIV-1	iso
135	27	93.1	297	10	AY203680	AY203680	HIV-1	iso
136	27	93.1	297	10	AY203681	AY203681	HIV-1	iso
137	27	93.1	297	10	AY203682	AY203682	HIV-1	iso
138	27	93.1	297	10	AY203683	AY203683	HIV-1	iso
139	27	93.1	297	10	AY203685	AY203685	HIV-1	iso
140	27	93.1	297	10	AY203687	AY203687	HIV-1	iso
141	27	93.1	297	10	AY203688	AY203688	HIV-1	iso
142	27	93.1	297	10	AY203689	AY203689	HIV-1	iso
143	27	93.1	297	10	AY305996	AY305996	HIV-1	iso
144	27	93.1	297	10	AY305999	AY305999	HIV-1	iso
145	27	93.1	297	10	AY313344	AY313344	HIV-1	iso
146	27	93.1	297	10	AY370055	AY370055	HIV-1	iso
147	27	93.1	297	10	AY370057	AY370057	HIV-1	iso
148	27	93.1	297	10	AY455412	AY455412	HIV-1	iso
149	27	93.1	297	10	AY502098	AY502098	HIV-1	iso
150	27	93.1	297	10	AY569833	AY569833	HIV-1	iso

ALIGNMENTS

RESULT 1

FCU06650

LOCUS FCU06650 658 bp RNA linear VRL 24-MAY-1995

DEFINITION Feline calicivirus FS capsid protein gene, partial cds.

ACCESSION U06650

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